

## SEQUENCE LISTING

&lt;110&gt; Alitalo et al

&lt;120&gt; VEGF-C OR VEGF-D MATERIALS AND METHODS FOR OLIGODENDROCYTES

&lt;130&gt; 28967/39670A

&lt;160&gt; 38

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 2772

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2772)

&lt;400&gt; 1

atg	gag	agg	ggg	ctg	ccg	ctc	ctc	tgc	gcc	gtg	ctc	gcc	ctc	gtc	ctc	48
Met	Glu	Arg	Gly	Leu	Pro	Leu	Leu	Cys	Ala	Val	Leu	Ala	Leu	Val	Leu	
1			5						10				15			

gcc	ccg	gcc	ggc	gct	ttt	cgc	aac	gat	gaa	tgt	ggc	gat	act	ata	aaa	96
Ala	Pro	Ala	Gly	Ala	Phe	Arg	Asn	Asp	Glu	Cys	Gly	Asp	Thr	Ile	Lys	
			20					25					30			

att	gaa	agc	ccc	ggg	tac	ctt	aca	tct	cct	ggg	tat	cct	cat	tct	tat	144
Ile	Glu	Ser	Pro	Gly	Tyr	Leu	Thr	Ser	Pro	Gly	Tyr	Pro	His	Ser	Tyr	
		35				40						45				

cac	cca	agt	gaa	aaa	tgc	gaa	tgg	ctg	att	cag	gct	ccg	gac	cca	tac	192
His	Pro	Ser	Glu	Lys	Cys	Glu	Trp	Leu	Ile	Gln	Ala	Pro	Asp	Pro	Tyr	
		50				55					60					

cag	aga	att	atg	atc	aac	ttc	aac	cct	cac	ttc	gat	ttg	gag	gac	aga	240
Gln	Arg	Ile	Met	Ile	Asn	Phe	Asn	Pro	His	Phe	Asp	Leu	Glu	Asp	Arg	
65					70					75					80	

gac	tgc	aag	tat	gac	tac	gtg	gaa	gtc	ttc	gat	gga	gaa	aat	gaa	aat	288
Asp	Cys	Lys	Tyr	Asp	Tyr	Val	Glu	Val	Phe	Asp	Gly	Glu	Asn	Glu	Asn	
				85				90						95		

gga	cat	ttt	agg	gga	aag	ttc	tgt	gga	aag	ata	gcc	cct	cct	cct	gtt	336
Gly	His	Phe	Arg	Gly	Lys	Phe	Cys	Gly	Lys	Ile	Ala	Pro	Pro	Pro	Val	
			100					105					110			

gtg	tct	tca	ggg	cca	ttt	ctt	ttt	atc	aaa	ttt	gtc	tct	gac	tac	gaa	384
Val	Ser	Ser	Gly	Pro	Phe	Leu	Phe	Ile	Lys	Phe	Val	Ser	Asp	Tyr	Glu	
		115				120							125			

aca	cat	ggg	gca	gga	ttt	tcc	ata	cgt	tat	gaa	att	ttc	aag	aga	ggg	432
Thr	His	Gly	Ala	Gly	Phe	Ser	Ile	Arg	Tyr	Glu	Ile	Phe	Lys	Arg	Gly	
		130				135					140					

cct	gaa	tgt	tcc	cag	aac	tac	aca	aca	cct	agt	gga	gtg	ata	aag	tcc	480
Pro	Glu	Cys	Ser	Gln	Asn	Tyr	Thr	Thr	Pro	Ser	Gly	Val	Ile	Lys	Ser	
145					150					155					160	

ccc gga ttc cct gaa aaa tat ccc aac agc ctt gaa tgc act tat att Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile 165 170 175	528
gtc ttt gcg cca aag atg tca gag att atc ctg gaa ttt gaa agc ttt Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe 180 185 190	576
gac ctg gag cct gac tca aat cct cca ggg ggg atg ttc tgt cgc tac Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr 195 200 205	624
gac cgg cta gaa atc tgg gat gga ttc cct gat gtt ggc cct cac att Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile 210 215 220	672
ggg cgt tac tgt gga cag aaa aca cca ggt cga atc cga tcc tca tcg Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser 225 230 235 240	720
ggc att ctc tcc atg gtt ttt tac acc gac agc gcg ata gca aaa gaa Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu 245 250 255	768
ggt ttc tca gca aac tac agt gtc ttg cag agc agt gtc tca gaa gat Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp 260 265 270	816
ttc aaa tgt atg gaa gct ctg ggc atg gaa tca gga gaa att cat tct Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser 275 280 285	864
gac cag atc aca gct tct tcc cag tat agc acc aac tgg tct gca gag Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu 290 295 300	912
cgc tcc cgc ctg aac tac cct gag aat ggg tgg act ccc gga gag gat Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp 305 310 315 320	960
tcc tac cga gag tgg ata cag gta gac ttg ggc ctt ctg cgc ttt gtc Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val 325 330 335	1008
acg gct gtc ggg aca cag ggc gcc att tca aaa gaa acc aag aag aaa Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys 340 345 350	1056
tat tat gtc aag act tac aag atc gac gtt agc tcc aac ggg gaa gac Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp 355 360 365	1104
tgg atc acc ata aaa gaa gga aac aaa cct gtt ctc ttt cag gga aac Trp Ile Thr Ile Lys Glu Gly Asn Lys Pro Val Leu Phe Gln Gly Asn 370 375 380	1152
acc aac ccc aca gat gtt gtg gtt gca gta ttc ccc aaa cca ctg ata Thr Asn Pro Thr Asp Val Val Val Ala Val Phe Pro Lys Pro Leu Ile 385 390 395 400	1200
act cga ttt gtc cga atc aag cct gca act tgg gaa act ggc ata tct Thr Arg Phe Val Arg Ile Lys Pro Ala Thr Trp Glu Thr Gly Ile Ser 405 410 415	1248

atg aga ttt gaa gta tac ggt tgc aag ata aca gat tat cct tgc tct Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser 420 425 430	1296
gga atg ttg ggt atg gtg tct gga ctt att tct gac tcc cag atc aca Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr 435 440 445	1344
tca tcc aac caa gga gac aga aac tgg atg cct gaa aac atc cgc ctg Ser Ser Asn Gln Gly Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu 450 455 460	1392
gta acc agt cgc tct ggc tgg gca ctt cca ccc gca cct cat tcc tac Val Thr Ser Arg Ser Gly Trp Ala Leu Pro Pro Ala Pro His Ser Tyr 465 470 475 480	1440
atc aat gag tgg ctc caa ata gac ctg ggg gag gag aag atc gtg agg Ile Asn Glu Trp Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile Val Arg 485 490 495	1488
ggc atc atc att cag ggt ggg aag cac cga gag aac aag gtg ttc atg Gly Ile Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met 500 505 510	1536
agg aag ttc aag atc ggg tac agc aac aac ggc tcg gac tgg aag atg Arg Lys Phe Lys Ile Gly Tyr Ser Asn Asn Gly Ser Asp Trp Lys Met 515 520 525	1584
atc atg gat gac agc aaa cgc aag gcg aag tct ttt gag ggc aac aac Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn 530 535 540	1632
aac tat gat aca cct gag ctg cgg act ttt cca gct ctc tcc acg cga Asn Tyr Asp Thr Pro Glu Leu Arg Thr Phe Pro Ala Leu Ser Thr Arg 545 550 555 560	1680
ttc atc agg atc tac ccc gag aga gcc act cat ggc gga ctg ggg ctc Phe Ile Arg Ile Tyr Pro Glu Arg Ala Thr His Gly Gly Leu Gly Leu 565 570 575	1728
aga atg gag ctg ctg ggc tgt gaa gtg gaa gcc cct aca gct gga ccg Arg Met Glu Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro 580 585 590	1776
acc act ccc aac ggg aac ttg gtg gat gaa tgt gat gac gac cag gcc Thr Thr Pro Asn Gly Asn Leu Val Asp Glu Cys Asp Asp Asp Gln Ala 595 600 605	1824
aac tgc cac agt gga aca ggt gat gac ttc cag ctc aca ggt ggc acc Asn Cys His Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr 610 615 620	1872
act gtg ctg gcc aca gaa aag ccc acg gtc ata gac agc acc ata caa Thr Val Leu Ala Thr Glu Lys Pro Thr Val Ile Asp Ser Thr Ile Gln 625 630 635 640	1920
tca gag ttt cca aca tat ggt ttt aac tgt gaa ttt ggc tgg ggc tct Ser Glu Phe Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser 645 650 655	1968
cac aag acc ttc tgc cac tgg gaa cat gac aat cac gtg cag ctc aag His Lys Thr Phe Cys His Trp Glu His Asp Asn His Val Gln Leu Lys 660 665 670	2016

tgg agt gtg ttg acc agc aag acg gga ccc att cag gat cac aca gga	2064
Trp Ser Val Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly	
675 680 685	
gat ggc aac ttc atc tat tcc caa gct gac gaa aat cag aag ggc aaa	2112
Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys	
690 695 700	
gtg gct cgc ctg gtg agc cct gtg gtt tat tcc cag aac tct gcc cac	2160
Val Ala Arg Leu Val Ser Pro Val Val Tyr Ser Gln Asn Ser Ala His	
705 710 715 720	
tgc atg acc ttc tgg tat cac atg tct ggg tcc cac gtc ggc aca ctc	2208
Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu	
725 730 735	
agg gtc aaa ctg cgc tac cag aag cca gag gag tac gat cag ctg gtc	2256
Arg Val Lys Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val	
740 745 750	
tgg atg gcc att gga cac caa ggt gac cac tgg aag gaa ggg cgt gtc	2304
Trp Met Ala Ile Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val	
755 760 765	
ttg ctc cac aag tct ctg aaa ctt tat cag gtg att ttc gag ggc gaa	2352
Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu	
770 775 780	
atc gga aaa gga aac ctt ggt ggg att gct gtg gat gac att agt att	2400
Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile	
785 790 795 800	
aat aac cac att tca caa gaa gat tgt gca aaa cca gca gac ctg gat	2448
Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Ala Asp Leu Asp	
805 810 815	
aaa aag aac cca gaa att aaa att gat gaa aca ggg agc acg cca gga	2496
Lys Lys Asn Pro Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly	
820 825 830	
tac gaa ggt gaa gga gaa ggt gac aag aac atc tcc agg aag cca ggc	2544
Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly	
835 840 845	
aat gtg ttg aag acc tta gaa ccc atc ctc atc acc atc ata gcc atg	2592
Asn Val Leu Lys Thr Leu Glu Pro Ile Leu Ile Thr Ile Ile Ala Met	
850 855 860	
agc gcc ctg ggg gtc ctc ctg ggg gct gtc tgt ggg gtc gtg ctg tac	2640
Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr	
865 870 875 880	
tgt gcc tgt tgg cat aat ggg atg tca gaa aga aac ttg tct gcc ctg	2688
Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu	
885 890 895	
gag aac tat aac ttt gaa ctt gtg gat ggt gtg aag ttg aaa aaa gac	2736
Glu Asn Tyr Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp	
900 905 910	
aaa ctg aat aca cag agt act tat tcg gag gca tga	2772
Lys Leu Asn Thr Gln Ser Thr Tyr Ser Glu Ala	
915 920	

<210> 2  
 <211> 923  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu  
 1 5 10 15

Ala Pro Ala Gly Ala Phe Arg Asn Asp Glu Cys Gly Asp Thr Ile Lys  
 20 25 30

Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr  
 35 40 45

His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr  
 50 55 60

Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg  
 65 70 75 80

Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn  
 85 90 95

Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Val  
 100 105 110

Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu  
 115 120 125

Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly  
 130 135 140

Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser  
 145 150 155 160

Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile  
 165 170 175

Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe  
 180 185 190

Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr  
 195 200 205

Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile  
 210 215 220

Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser  
 225 230 235 240

Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu  
 245 250 255

Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp  
 260 265 270

Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser  
 275 280 285

Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu  
 290 295 300

Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp  
 305 310 315 320

Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val  
 325 330 335

Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys  
 340 345 350

Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp  
 355 360 365

Trp Ile Thr Ile Lys Glu Gly Asn Lys Pro Val Leu Phe Gln Gly Asn  
 370 375 380

Thr Asn Pro Thr Asp Val Val Val Ala Val Phe Pro Lys Pro Leu Ile  
 385 390 395 400

Thr Arg Phe Val Arg Ile Lys Pro Ala Thr Trp Glu Thr Gly Ile Ser  
 405 410 415

Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser  
 420 425 430

Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr  
 435 440 445

Ser Ser Asn Gln Gly Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu  
 450 455 460

Val Thr Ser Arg Ser Gly Trp Ala Leu Pro Pro Ala Pro His Ser Tyr  
 465 470 475 480

Ile Asn Glu Trp Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile Val Arg  
 485 490 495

Gly Ile Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met  
 500 505 510

Arg Lys Phe Lys Ile Gly Tyr Ser Asn Asn Gly Ser Asp Trp Lys Met  
 515 520 525

Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn  
 530 535 540

Asn Tyr Asp Thr Pro Glu Leu Arg Thr Phe Pro Ala Leu Ser Thr Arg  
 545 550 555 560

Phe Ile Arg Ile Tyr Pro Glu Arg Ala Thr His Gly Gly Leu Gly Leu  
 565 570 575

Arg Met Glu Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro  
 580 585 590

Thr Thr Pro Asn Gly Asn Leu Val Asp Glu Cys Asp Asp Asp Gln Ala  
 595 600 605

Asn Cys His Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr  
 610 615 620

Thr Val Leu Ala Thr Glu Lys Pro Thr Val Ile Asp Ser Thr Ile Gln  
 625 630 635 640

Ser Glu Phe Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser  
 645 650 655

His Lys Thr Phe Cys His Trp Glu His Asp Asn His Val Gln Leu Lys  
 660 665 670

Trp Ser Val Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly  
 675 680 685

Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys  
 690 695 700

Val Ala Arg Leu Val Ser Pro Val Val Tyr Ser Gln Asn Ser Ala His  
 705 710 715 720

Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu  
725 730 735

Arg Val Lys Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val  
740 745 750

Trp Met Ala Ile Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val  
755 760 765

Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu  
770 775 780

Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile  
785 790 795 800

Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Ala Asp Leu Asp  
805 810 815

Lys Lys Asn Pro Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly  
820 825 830

Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly  
835 840 845

Asn Val Leu Lys Thr Leu Glu Pro Ile Leu Ile Thr Ile Ile Ala Met  
850 855 860

Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr  
865 870 875 880

Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu  
885 890 895

Glu Asn Tyr Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp  
900 905 910

Lys Leu Asn Thr Gln Ser Thr Tyr Ser Glu Ala  
915 920

<210> 3  
<211> 2781  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(2781)



WO 2005/030240

<400> 3  
 atg gat atg ttt cct ctc acc tgg gtt ttc tta gcc ctc tac ttt tca 48  
 Met Asp Met Phe Pro Leu Thr Trp Val Phe Leu Ala Leu Tyr Phe Ser 15  
 1 5 10

aga cac caa gtg aga ggc caa cca gac cca ccg tgc gga ggt cgt ttg 96  
 Arg His Gln Val Arg Gly Gln Pro Asp Pro Pro Cys Gly Gly Arg Leu 30  
 20 25

aat tcc aaa gat gct ggc tat atc acc tct ccc ggt tac ccc cag gac 144  
 Asn Ser Lys Asp Ala Gly Tyr Ile Thr Ser Pro Gly Tyr Pro Gln Asp 45  
 35 40

tac ccc tcc cac cag aac tgc gag tgg att gtt tac gcc ccc gaa ccc 192  
 Tyr Pro Ser His Gln Asn Cys Glu Trp Ile Val Tyr Ala Pro Glu Pro 60  
 50 55

aac cag aag att gtc ctc aac ttc aac cct cac ttt gaa atc gag aag 240  
 Asn Gln Lys Ile Val Leu Asn Phe Asn Pro His Phe Glu Ile Glu Lys 80  
 65 70 75

cac gac tgc aag tat gac ttt atc gag att cgg gat ggg gac agt gaa 288  
 His Asp Cys Lys Tyr Asp Phe Ile Glu Ile Arg Asp Gly Asp Ser Glu 95  
 85 90

tcc gca gac ctc ctg ggc aaa cac tgt ggg aac atc gcc ccg ccc acc 336  
 Ser Ala Asp Leu Leu Gly Lys His Cys Gly Asn Ile Ala Pro Pro Thr 110  
 100 105

atc atc tcc tcg ggc tcc atg ctc tac atc aag ttc acc tcc gac tac 384  
 Ile Ile Ser Ser Gly Ser Met Leu Tyr Ile Lys Phe Thr Ser Asp Tyr 125  
 115 120

gcc cgg cag ggg gca ggc ttc tct ctg cgc tac gag atc ttc aag aca 432  
 Ala Arg Gln Gly Ala Gly Phe Ser Leu Arg Tyr Glu Ile Phe Lys Thr 140  
 130 135

ggc tct gaa gat tgc tca aaa aac ttc aca agc ccc aac ggg acc atc 480  
 Gly Ser Glu Asp Cys Ser Lys Asn Phe Thr Ser Pro Asn Gly Thr Ile 160  
 145 150 155

gaa tct cct ggg ttt cct gag aag tat cca cac aac ttg gac tgc acc 528  
 Glu Ser Pro Gly Phe Pro Glu Lys Tyr Pro His Asn Leu Asp Cys Thr 175  
 165 170

ttt acc atc ctg gcc aaa ccc aag atg gag atc atc ctg cag ttc ctg 576  
 Phe Thr Ile Leu Ala Lys Pro Lys Met Glu Ile Ile Leu Gln Phe Leu 190  
 180 185

atc ttt gac ctg gag cat gac cct ttg cag gtg gga gag ggg gac tgc 624  
 Ile Phe Asp Leu Glu His Asp Pro Leu Gln Val Gly Glu Gly Asp Cys 205  
 195 200

aag tac gat tgg ctg gac atc tgg gat ggc att cca cat gtt ggc ccc 672  
 Lys Tyr Asp Trp Leu Asp Ile Trp Asp Gly Ile Pro His Val Gly Pro 220  
 210 215

ctg att ggc aag tac tgt ggg acc aaa aca ccc tct gaa ctt cgt tca 720  
 Leu Ile Gly Lys Tyr Cys Gly Thr Lys Thr Pro Ser Glu Leu Arg Ser 240  
 225 230 235

tcg acg ggg atc ctc tcc ctg acc ttt cac acg gac atg gcg gtg gcc Ser Thr Gly Ile Leu Ser Leu Thr Phe His Thr Asp Met Ala Val Ala 245 250 255	768
aag gat ggc ttc tct gcg cgt tac tac ctg gtc cac caa gag cca cta Lys Asp Gly Phe Ser Ala Arg Tyr Tyr Leu Val His Gln Glu Pro Leu 260 265 270	816
gag aac ttt cag tgc aat gtt cct ctg ggc atg gag tct ggc cgg att Glu Asn Phe Gln Cys Asn Val Pro Leu Gly Met Glu Ser Gly Arg Ile 275 280 285	864
gct aat gaa cag atc agt gcc tca tct acc tac tct gat ggg agg tgg Ala Asn Glu Gln Ile Ser Ala Ser Ser Thr Tyr Ser Asp Gly Arg Trp 290 295 300	912
acc cct caa caa agc cgg ctc cat ggt gat gac aat ggc tgg acc ccc Thr Pro Gln Gln Ser Arg Leu His Gly Asp Asn Gly Trp Thr Pro 305 310 315 320	960
aac ttg gat tcc aac aag gag tat ctc cag gtg gac ctg cgc ttt tta Asn Leu Asp Ser Asn Lys Glu Tyr Leu Gln Val Asp Leu Arg Phe Leu 325 330 335	1008
acc atg ctc acg gcc atc gca aca cag gga gcg att tcc agg gaa aca Thr Met Leu Thr Ala Ile Ala Thr Gln Gly Ala Ile Ser Arg Glu Thr 340 345 350	1056
cag aat ggc tac tac gtc aaa tcc tac aag ctg gaa gtc agc act aat Gln Asn Gly Tyr Tyr Val Lys Ser Tyr Lys Leu Glu Val Ser Thr Asn 355 360 365	1104
gga gag gac tgg atg gtg tac cgg cat ggc aaa aac cac aag gta ttt Gly Glu Asp Trp Met Val Tyr Arg His Gly Lys Asn His Lys Val Phe 370 375 380	1152
caa gcc aac aac gat gca act gag gtg gtt ctg aac aag ctc cac gct Gln Ala Asn Asn Asp Ala Thr Glu Val Val Leu Asn Lys Leu His Ala 385 390 395 400	1200
cca ctg ctg aca agg ttt gtt aga atc cgc cct cag acc tgg cac tca Pro Leu Leu Thr Arg Phe Val Arg Ile Arg Pro Gln Thr Trp His Ser 405 410 415	1248
ggt atc gcc ctc cgg ctg gag ctc ttc ggc tgc cgg gtc aca gat gct Gly Ile Ala Leu Arg Leu Glu Leu Phe Gly Cys Arg Val Thr Asp Ala 420 425 430	1296
ccc tgc tcc aac atg ctg ggg atg ctc tca ggc ctc att gca gac tcc Pro Cys Ser Asn Met Leu Gly Met Leu Ser Gly Leu Ile Ala Asp Ser 435 440 445	1344
cag atc tcc gcc tct tcc acc cag gaa tac ctc tgg agc ccc agt gca Gln Ile Ser Ala Ser Ser Thr Gln Glu Tyr Leu Trp Ser Pro Ser Ala 450 455 460	1392
gcc cgc ctg gtc agc agc cgc tcg ggc tgg ttc cct cga atc cct cag Ala Arg Leu Val Ser Arg Ser Gly Trp Phe Pro Arg Ile Pro Gln 465 470 475 480	1440
gcc cag ccc ggt gag gag tgg ctt cag gta gat ctg gga aca ccc aag Ala Gln Pro Gly Glu Glu Trp Leu Gln Val Asp Leu Gly Thr Pro Lys 485 490 495	1488

aca gtg aaa ggt gtc atc atc cag gga gcc cgc gga gga gac agt atc Thr Val Lys Gly Val Ile Ile Gln Gly Ala Arg Gly Gly Asp Ser Ile 500 505 510	1536
act gct gtg gaa gcc aga gca ttt gtg cgc aag ttc aaa gtc tcc tac Thr Ala Val Glu Ala Arg Ala Phe Val Arg Lys Phe Lys Val Ser Tyr 515 520 525	1584
agc cta aac ggc aag gac tgg gaa tac att cag gac ccc agg acc cag Ser Leu Asn Gly Lys Asp Trp Glu Tyr Ile Gln Asp Pro Arg Thr Gln 530 535 540	1632
cag cca aag ctg ttc gaa ggg aac atg cac tat gac acc cct gac atc Gln Pro Lys Leu Phe Glu Gly Asn Met His Tyr Asp Thr Pro Asp Ile 545 550 555 560	1680
cga agg ttt gac ccc att ccg gca cag tat gtg cgg gta tac ccg gag Arg Arg Phe Asp Pro Ile Pro Ala Gln Tyr Val Arg Val Tyr Pro Glu 565 570 575	1728
agg tgg tcg ccg gcg ggg att ggg atg cgg ctg gag gtg ctg ggc tgt Arg Trp Ser Pro Ala Gly Ile Gly Met Arg Leu Glu Val Leu Gly Cys 580 585 590	1776
gac tgg aca gac tcc aag ccc acg gta aaa acg ctg gga ccc act gtg Asp Trp Thr Asp Ser Lys Pro Thr Val Lys Thr Leu Gly Pro Thr Val 595 600 605	1824
aag agc gaa gag aca acc acc ccc tac ccc acc gaa gag gag gcc aca Lys Ser Glu Glu Thr Thr Thr Pro Tyr Pro Thr Glu Glu Glu Ala Thr 610 615 620	1872
gag tgt ggg gag aac tgc agc ttt gag gat gac aaa gat ttg cag ctc Glu Cys Gly Glu Asn Cys Ser Phe Glu Asp Asp Lys Asp Leu Gln Leu 625 630 635 640	1920
cct tcg gga ttc aat tgc aac ttc gat ttc ctc gag gag ccc tgt ggt Pro Ser Gly Phe Asn Cys Asn Phe Asp Phe Leu Glu Glu Pro Cys Gly 645 650 655	1968
tgg atg tat gac cat gcc aag tgg ctc cgg acc acc tgg gcc agc agc Trp Met Tyr Asp His Ala Lys Trp Leu Arg Thr Thr Trp Ala Ser Ser 660 665 670	2016
tcc agc cca aac gac cgg acg ttt cca gat gac agg aat ttc ttg cgg Ser Ser Pro Asn Asp Arg Thr Phe Pro Asp Asp Arg Asn Phe Leu Arg 675 680 685	2064
ctg cag agt gac agc cag aga gag ggc cag tat gcc cgg ctc atc agc Leu Gln Ser Asp Ser Gln Arg Glu Gly Gln Tyr Ala Arg Leu Ile Ser 690 695 700	2112
ccc cct gtc cac ctg ccc cga agc ccg gtg tgc atg gag ttc cag tac Pro Pro Val His Leu Pro Arg Ser Pro Val Cys Met Glu Phe Gln Tyr 705 710 715 720	2160
cag gcc acg ggc ggc cgc ggg gtg gcg ctg cag gtg gtg cgg gaa gcc Gln Ala Thr Gly Gly Arg Gly Val Ala Leu Gln Val Val Arg Glu Ala 725 730 735	2208
agc cag gag agc aag ttg ctg tgg gtc atc cgt gag gac cag ggc ggc Ser Gln Glu Ser Lys Leu Leu Trp Val Ile Arg Glu Asp Gln Gly Gly 740 745 750	2256

gag tgg aag cac ggg cgg atc atc ctg ccc agc tac gac atg gag tac 2304  
 Glu Trp Lys His Gly Arg Ile Ile Leu Pro Ser Tyr Asp Met Glu Tyr  
 755 760 765  
 cag att gtg ttc gag gga gtg ata ggg aaa gga cgt tcc gga gag att 2352  
 Gln Ile Val Phe Glu Gly Val Ile Gly Lys Gly Arg Ser Gly Glu Ile  
 770 775 780  
 gcc att gat gac att cgg ata agc act gat gtc cca ctg gag aac tgc 2400  
 Ala Ile Asp Asp Ile Arg Ile Ser Thr Asp Val Pro Leu Glu Asn Cys  
 785 790 795 800  
 atg gaa ccc atc tcg gct ttt gca gtg gac atc cca gaa ata cat gag 2448  
 Met Glu Pro Ile Ser Ala Phe Ala Val Asp Ile Pro Glu Ile His Glu  
 805 810 815  
 aga gaa gga tat gaa gat gaa att gat gat gaa tac gag gtg gac tgg 2496  
 Arg Glu Gly Tyr Glu Asp Glu Ile Asp Asp Glu Tyr Glu Val Asp Trp  
 820 825 830  
 agc aat tct tct tct gca acc tca ggg tct ggc gcc ccc tcg acc gac 2544  
 Ser Asn Ser Ser Ser Ala Thr Ser Gly Ser Gly Ala Pro Ser Thr Asp  
 835 840 845  
 aaa gaa aag agc tgg ctg tac acc ctg gat ccc atc ctc atc acc atc 2592  
 Lys Glu Lys Ser Trp Leu Tyr Thr Leu Asp Pro Ile Leu Ile Thr Ile  
 850 855 860  
 atc gcc atg agc tca ctg ggc gtc ctc ctg ggg gcc acc tgt gca ggc 2640  
 Ile Ala Met Ser Ser Leu Gly Val Leu Leu Gly Ala Thr Cys Ala Gly  
 865 870 875 880  
 ctc ctg ctc tac tgc acc tgt tcc tac tcg ggc ctg agc tcc cga agc 2688  
 Leu Leu Leu Tyr Cys Thr Cys Ser Tyr Ser Gly Leu Ser Ser Arg Ser  
 885 890 895  
 tgc acc aca ctg gag aac tac aac ttc gag ctc tac gat ggc ctt aag 2736  
 Cys Thr Thr Leu Glu Asn Tyr Asn Phe Glu Leu Tyr Asp Gly Leu Lys  
 900 905 910  
 cac aag gtc aag atg aac cac caa aag tgc tgc tcc gag gca tga 2781  
 His Lys Val Lys Met Asn His Gln Lys Cys Cys Ser Glu Ala  
 915 920 925

<210> 4  
 <211> 926  
 <212> PRT  
 <213> Homo sapiens  
 <400> 4

Met Asp Met Phe Pro Leu Thr Trp Val Phe Leu Ala Leu Tyr Phe Ser  
 1 5 10 15

Arg His Gln Val Arg Gly Gln Pro Asp Pro Pro Cys Gly Gly Arg Leu  
 20 25 30

Asn Ser Lys Asp Ala Gly Tyr Ile Thr Ser Pro Gly Tyr Pro Gln Asp  
 35 40 45

Tyr Pro Ser His Gln Asn Cys Glu Trp Ile Val Tyr Ala Pro Glu Pro  
 50 55 60

Asn Gln Lys Ile Val Leu Asn Phe Asn Pro His Phe Glu Ile Glu Lys  
 65 70 75 80

His Asp Cys Lys Tyr Asp Phe Ile Glu Ile Arg Asp Gly Asp Ser Glu  
 85 90 95

Ser Ala Asp Leu Leu Gly Lys His Cys Gly Asn Ile Ala Pro Pro Thr  
 100 105 110

Ile Ile Ser Ser Gly Ser Met Leu Tyr Ile Lys Phe Thr Ser Asp Tyr  
 115 120 125

Ala Arg Gln Gly Ala Gly Phe Ser Leu Arg Tyr Glu Ile Phe Lys Thr  
 130 135 140

Gly Ser Glu Asp Cys Ser Lys Asn Phe Thr Ser Pro Asn Gly Thr Ile  
 145 150 155 160

Glu Ser Pro Gly Phe Pro Glu Lys Tyr Pro His Asn Leu Asp Cys Thr  
 165 170 175

Phe Thr Ile Leu Ala Lys Pro Lys Met Glu Ile Ile Leu Gln Phe Leu  
 180 185 190

Ile Phe Asp Leu Glu His Asp Pro Leu Gln Val Gly Glu Gly Asp Cys  
 195 200 205

Lys Tyr Asp Trp Leu Asp Ile Trp Asp Gly Ile Pro His Val Gly Pro  
 210 215 220

Leu Ile Gly Lys Tyr Cys Gly Thr Lys Thr Pro Ser Glu Leu Arg Ser  
 225 230 235 240

Ser Thr Gly Ile Leu Ser Leu Thr Phe His Thr Asp Met Ala Val Ala  
 245 250 255

Lys Asp Gly Phe Ser Ala Arg Tyr Tyr Leu Val His Gln Glu Pro Leu  
 260 265 270

Glu Asn Phe Gln Cys Asn Val Pro Leu Gly Met Glu Ser Gly Arg Ile  
 275 280 285

Ala Asn Glu Gln Ile Ser Ala Ser Ser Thr Tyr Ser Asp Gly Arg Trp  
 290 295 300

Thr Pro Gln Gln Ser Arg Leu His Gly Asp Asp Asn Gly Trp Thr Pro  
 305 310 315 320  
 Asn Leu Asp Ser Asn Lys Glu Tyr Leu Gln Val Asp Leu Arg Phe Leu  
 325 330 335  
 Thr Met Leu Thr Ala Ile Ala Thr Gln Gly Ala Ile Ser Arg Glu Thr  
 340 345 350  
 Gln Asn Gly Tyr Tyr Val Lys Ser Tyr Lys Leu Glu Val Ser Thr Asn  
 355 360 365  
 Gly Glu Asp Trp Met Val Tyr Arg His Gly Lys Asn His Lys Val Phe  
 370 375 380  
 Gln Ala Asn Asn Asp Ala Thr Glu Val Val Leu Asn Lys Leu His Ala  
 385 390 395 400  
 Pro Leu Leu Thr Arg Phe Val Arg Ile Arg Pro Gln Thr Trp His Ser  
 405 410 415  
 Gly Ile Ala Leu Arg Leu Glu Leu Phe Gly Cys Arg Val Thr Asp Ala  
 420 425 430  
 Pro Cys Ser Asn Met Leu Gly Met Leu Ser Gly Leu Ile Ala Asp Ser  
 435 440 445  
 Gln Ile Ser Ala Ser Ser Thr Gln Glu Tyr Leu Trp Ser Pro Ser Ala  
 450 455 460  
 Ala Arg Leu Val Ser Ser Arg Ser Gly Trp Phe Pro Arg Ile Pro Gln  
 465 470 475 480  
 Ala Gln Pro Gly Glu Glu Trp Leu Gln Val Asp Leu Gly Thr Pro Lys  
 485 490 495  
 Thr Val Lys Gly Val Ile Ile Gln Gly Ala Arg Gly Gly Asp Ser Ile  
 500 505 510  
 Thr Ala Val Glu Ala Arg Ala Phe Val Arg Lys Phe Lys Val Ser Tyr  
 515 520 525  
 Ser Leu Asn Gly Lys Asp Trp Glu Tyr Ile Gln Asp Pro Arg Thr Gln  
 530 535 540  
 Gln Pro Lys Leu Phe Glu Gly Asn Met His Tyr Asp Thr Pro Asp Ile  
 545 550 555 560

Arg Arg Phe Asp Pro Ile Pro Ala Gln Tyr Val Arg Val Tyr Pro Glu  
 565 570 575

Arg Trp Ser Pro Ala Gly Ile Gly Met Arg Leu Glu Val Leu Gly Cys  
 580 585 590

Asp Trp Thr Asp Ser Lys Pro Thr Val Lys Thr Leu Gly Pro Thr Val  
 595 600 605

Lys Ser Glu Glu Thr Thr Thr Pro Tyr Pro Thr Glu Glu Glu Ala Thr  
 610 615 620

Glu Cys Gly Glu Asn Cys Ser Phe Glu Asp Asp Lys Asp Leu Gln Leu  
 625 630 635 640

Pro Ser Gly Phe Asn Cys Asn Phe Asp Phe Leu Glu Glu Pro Cys Gly  
 645 650 655

Trp Met Tyr Asp His Ala Lys Trp Leu Arg Thr Thr Trp Ala Ser Ser  
 660 665 670

Ser Ser Pro Asn Asp Arg Thr Phe Pro Asp Asp Arg Asn Phe Leu Arg  
 675 685

Leu Gln Ser Asp Ser Gln Arg Glu Gly Gln Tyr Ala Arg Leu Ile Ser  
 690 695 700

Pro Pro Val His Leu Pro Arg Ser Pro Val Cys Met Glu Phe Gln Tyr  
 705 710 715 720

Gln Ala Thr Gly Gly Arg Gly Val Ala Leu Gln Val Val Arg Glu Ala  
 725 730 735

Ser Gln Glu Ser Lys Leu Leu Trp Val Ile Arg Glu Asp Gln Gly Gly  
 740 745 750

Glu Trp Lys His Gly Arg Ile Ile Leu Pro Ser Tyr Asp Met Glu Tyr  
 755 760 765

Gln Ile Val Phe Glu Gly Val Ile Gly Lys Gly Arg Ser Gly Glu Ile  
 770 775 780

Ala Ile Asp Asp Ile Arg Ile Ser Thr Asp Val Pro Leu Glu Asn Cys  
 785 790 795 800

Met Glu Pro Ile Ser Ala Phe Ala Val Asp Ile Pro Glu Ile His Glu  
 805 810 815

Arg Glu Gly Tyr Glu Asp Glu Ile Asp Asp Glu Tyr Glu Val Asp Trp  
820 825 830

Ser Asn Ser Ser Ser Ala Thr Ser Gly Ser Gly Ala Pro Ser Thr Asp  
835 840 845

Lys Glu Lys Ser Trp Leu Tyr Thr Leu Asp Pro Ile Leu Ile Thr Ile  
850 855 860

Ile Ala Met Ser Ser Leu Gly Val Leu Leu Gly Ala Thr Cys Ala Gly  
865 870 875 880

Leu Leu Leu Tyr Cys Thr Cys Ser Tyr Ser Gly Leu Ser Ser Arg Ser  
885 890 895

Cys Thr Thr Leu Glu Asn Tyr Asn Phe Glu Leu Tyr Asp Gly Leu Lys  
900 905 910

His Lys Val Lys Met Asn His Gln Lys Cys Cys Ser Glu Ala  
915 920 925

<210> 5  
<211> 3652  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (348) .. (3119)

<220>  
<221> misc\_feature  
<222> (348) .. (410)  
<223> Signal Peptide

<400> 5.  
tttttttttt tttttttttt tttttttttt tttttctctc ttctttcttct tcttgagaca 60  
tggcccgggc agtggctcct ggaagaggaa caagtgtggg aaaagggaga ggaaatcgga 120  
gctaaatgac aggatgcagg cgacttgaga cacaaaaaga gaagcgcttc tcgcgaattc 180  
aggcattgcc tcgccgctag ccttccccgc caagaccgcg tgaggatttt atggttctta 240  
ggcggactta agagcgtttc ggattgttaa gattatcggt tgcgtggttt tcgtccgcgc 300  
aatcgtgttc tctgcggtt gcctggggac tggcttggcg aaggagg atg gag agg 356  
Met Glu Arg  
1

ggg ctg ccg ttg ctg tgc gcc acg ctc gcc ctt gcc ctc gcc ctg gcg 404  
Gly Leu Pro Leu Leu Cys Ala Thr Leu Ala Leu Ala Leu Ala  
5 10 15



ggc gct ttc cgc agc gac aaa tgt ggc ggg acc ata aaa atc gaa aac Gly Ala Phe Arg Ser Asp Lys Cys Gly Gly Thr Ile Lys Ile Glu Asn 20 25 30 35	452
cca ggg tac ctc aca tct ccc ggt tac cct cat tct tac cat cca agt Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr His Pro Ser 40 45 50	500
gag aag tgt gaa tgg cta atc caa gct ccg gaa ccc tac cag aga atc Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Glu Pro Tyr Gln Arg Ile 55 60 65	548
ata atc aac ttc aac cca cat ttc gat ttg gag gac aga gac tgc aag Ile Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg Asp Cys Lys 70 75 80	596
tat gac tac gtg gaa gta att gat ggg gag aat gaa ggc ggc cgc ctg Tyr Asp Tyr Val Glu Val Ile Asp Gly Glu Asn Glu Gly Gly Arg Leu 85 90 95	644
tgg ggg aag ttc tgt ggg aag att gca cct tct cct gtg gtg tct tca Trp Gly Lys Phe Cys Gly Lys Ile Ala Pro Ser Pro Val Val Ser Ser 100 105 110 115	692
ggg ccc ttt ctc ttc atc aaa ttt gtc tct gac tat gag aca cat ggg Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu Thr His Gly 120 125 130	740
gca ggg ttt tcc atc cgc tat gaa atc ttc aag aga ggg ccc gaa tgt Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly Pro Glu Cys 135 140 145	788
tct cag aac tat aca gca cct act gga gtg ata aag tcc cct ggg ttc Ser Gln Asn Tyr Thr Ala Pro Thr Gly Val Ile Lys Ser Pro Gly Phe 150 155 160	836
cct gaa aaa tac ccc aac tgc ttg gag tgc acc tac atc atc ttt gca Pro Glu Lys Tyr Pro Asn Cys Leu Glu Cys Thr Tyr Ile Ile Phe Ala 165 170 175	884
cca aag atg tct gag ata atc ctg gag ttt gaa agt ttt gac ctg gag Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe Asp Leu Glu 180 185 190 195	932
caa gac tcg aat cct ccc gga gga atg ttc tgt cgc tat gac cgg ctg Gln Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr Asp Arg Leu 200 205 210	980
gag atc tgg gat gga ttc cct gaa gtt ggc cct cac att ggg cgt tat Glu Ile Trp Asp Gly Phe Pro Glu Val Gly Pro His Ile Gly Arg Tyr 215 220 225	1028
tgt ggg cag aaa act cct ggc cgg atc cgc tcc tct tca ggc gtt cta Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser Gly Val Leu 230 235 240	1076
tcc atg gtc ttt tac act gac agc gca ata gca aaa gaa ggt ttc tca Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu Gly Phe Ser 245 250 255	1124
gcc aac tac agt gtg cta cag agc agc atc tct gaa gat ttt aag tgt Ala Asn Tyr Ser Val Leu Gln Ser Ser Ile Ser Glu Asp Phe Lys Cys 260 265 270 275	1172

atg gag gct ctg ggc atg gaa tct gga gag atc cat tct gat cag atc Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser Asp Gln Ile 280 285 290	1220
act gca tct tca cag tat ggt acc aac tgg tct gta gag cgc tcc cgc Thr Ala Ser Ser Gln Tyr Gly Thr Asn Trp Ser Val Glu Arg Ser Arg 295 300 305	1268
ctg aac tac cct gaa aat ggg tgg act cca gga gaa gac tcc tac aag Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp Ser Tyr Lys 310 315 320	1316
gag tgg atc cag gtg gac ttg ggc ctc ctg cga ttc gtt act gct gta Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val Thr Ala Val 325 330 335	1364
ggg aca cag ggt gcc att tcc aag gaa acc aag aag aaa tat tat gtc Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys Tyr Tyr Val 340 345 350 355	1412
aag act tac aga gta gac atc agc tcc aac gga gag gac tgg atc tcc Lys Thr Tyr Arg Val Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Ser 360 365 370	1460
ctg aaa gag gga aat aaa gcc att atc ttt cag gga aac acc aac ccc Leu Lys Glu Gly Asn Lys Ala Ile Ile Phe Gln Gly Asn Thr Asn Pro 375 380 385	1508
aca gat gtt gtc tta gga gtt ttc tcc aaa cca ctg ata act cga ttt Thr Asp Val Val Leu Gly Val Phe Ser Lys Pro Leu Ile Thr Arg Phe 390 395 400	1556
gtc cga atc aaa cct gta tcc tgg gaa act ggt ata tct atg aga ttt Val Arg Ile Lys Pro Val Ser Trp Glu Thr Gly Ile Ser Met Arg Phe 405 410 415	1604
gaa gtt tat ggc tgc aag ata aca gat tat cct tgc tct gga atg ttg Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser Gly Met Leu 420 425 430 435	1652
ggc atg gtg tct gga ctt att tca gac tcc cag att aca gca tcc aat Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr Ala Ser Asn 440 445 450	1700
caa gcc gac agg aat tgg atg cca gaa aac atc cgt ctg gtg acc agt Gln Ala Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu Val Thr Ser 455 460 465	1748
cgt acc ggc tgg gca ctg cca ccc tca ccc cac cca tac acc aat gaa Arg Thr Gly Trp Ala Leu Pro Pro Ser Pro His Pro Tyr Thr Asn Glu 470 475 480	1796
tgg ctc caa gtg gac ctg gga gat gag aag ata gta aga ggt gtc atc Trp Leu Gln Val Asp Leu Gly Asp Glu Lys Ile Val Arg Gly Val Ile 485 490 495	1844
att cag ggt ggg aag cac cga gaa aac aag gtg ttc atg agg aag ttc Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met Arg Lys Phe 500 505 510 515	1892
aag atc gcc tat agt aac aat ggc tct gac tgg aaa act atc atg gat Lys Ile Ala Tyr Ser Asn Asn Gly Ser Asp Trp Lys Thr Ile Met Asp 520 525 530	1940

gac agc aag cgc aag gct aag tgc ttc gaa ggc aac aac aac tat gac Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn Asn Tyr Asp 535 540 545	1988
aca cct gag ctt cgg acg ttt tca cct ctc tcc aca agg ttc atc agg Thr Pro Glu Leu Arg Thr Phe Ser Pro Leu Ser Thr Arg Phe Ile Arg 550 555 560	2036
atc tac cct gag aga gcc aca cac agt ggg ctt ggg ctg agg atg gag Ile Tyr Pro Glu Arg Ala Thr His Ser Gly Leu Gly Leu Arg Met Glu 565 570 575	2084
cta ctg ggc tgt gaa gtg gaa gca cct aca gct gga cca acc aca ccc Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro Thr Thr Pro 580 585 590 595	2132
aat ggg aac cca gtg cat gag tgt gac gac gac cag gcc aac tgc cac Asn Gly Asn Pro Val His Glu Cys Asp Asp Asp Gln Ala Asn Cys His 600 605 610	2180
agt ggc aca ggt gat gac ttc cag ctc aca gga ggc acc act gtc ctg Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr Thr Val Leu 615 620 625	2228
gcc aca gag aag cca acc att ata gac agc acc atc caa tca gag ttc Ala Thr Glu Lys Pro Thr Ile Ile Asp Ser Thr Ile Gln Ser Glu Phe 630 635 640	2276
ccg aca tac ggt ttt aac tgc gag ttt ggc tgg ggc tct cac aag aca Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser His Lys Thr 645 650 655	2324
ttc tgc cac tgg gag cat gac agc cat gca cag ctc agg tgg agt gtg Phe Cys His Trp Glu His Asp Ser His Ala Gln Leu Arg Trp Ser Val 660 665 670 675	2372
ctg acc agc aag aca ggg ccg att cag gac cat aca gga gat ggc aac Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly Asp Gly Asn 680 685 690	2420
ttc atc tat tcc caa gct gat gaa aat cag aaa ggc aaa gta gcc cgc Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys Val Ala Arg 695 700 705	2468
ctg gtg agc cct gtg gtc tat tcc cag agc tct gcc cac tgt atg acc Leu Val Ser Pro Val Val Tyr Ser Gln Ser Ser Ala His Cys Met Thr 710 715 720	2516
ttc tgg tat cac atg tcc ggc tct cat gtg ggt aca ctg agg gtc aaa Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu Arg Val Lys 725 730 735	2564
cta cgc tac cag aag cca gag gaa tat gat caa ctg gtc tgg atg gtg Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val Trp Met Val 740 745 750 755	2612
gtt ggg cac caa gga gac cac tgg aaa gaa gga cgt gtc ttg ctg cac Val Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val Leu Leu His 760 765 770	2660
aaa tct ctg aaa cta tat cag gtt att ttt gaa ggt gaa atc gga aaa Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu Ile Gly Lys 775 780 785	2708

gga aac ctt ggt gga att gct gtg gat gat atc agt att aac aac cat 2756  
 Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile Asn Asn His  
 790 795 800

att tct cag gaa gac tgt gca aaa cca aca gac cta gat aaa aag aac 2804  
 Ile Ser Gln Glu Asp Cys Ala Lys Pro Thr Asp Leu Asp Lys Lys Asn  
 805 810 815

aca gaa att aaa att gat gaa aca ggg agc act cca gga tat gaa gga 2852  
 Thr Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly Tyr Glu Gly  
 820 825 830 835

gaa ggg gaa ggt gac aag aac atc tcc agg aag cca ggc aat gtg ctt 2900  
 Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly Asn Val Leu  
 840 845 850

aag acc ctg gat ccc atc ctg atc acc atc ata gcc atg agt gcc ctg 2948  
 Lys Thr Leu Asp Pro Ile Leu Ile Thr Ile Ile Ala Met Ser Ala Leu  
 855 860 865

gga gta ctc ctg ggt gca gtc tgt gga gtt gtg ctg tac tgt gcc tgt 2996  
 Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr Cys Ala Cys  
 870 875 880

tgg cac aat ggg atg tca gaa agg aac cta tct gcc ctg gag aac tat 3044  
 Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu Glu Asn Tyr  
 885 890 895

aac ttt gaa ctt gtg gat ggt gta aag ttg aaa aaa gat aaa ctg aac 3092  
 Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp Lys Leu Asn  
 900 905 910 915

cca cag agt aat tac tca gag gcg tga aggcacggag ctggagggaa 3139  
 Pro Gln Ser Asn Tyr Ser Glu Ala  
 920

caagggagga gcacggcagg agaacagggtg gaggcacggg gactctgtta ctctgctttc 3199

actgtaagct gggaagggcg gggactctgt tactccgctt tcaactgtaag ctcggaaggg 3259

catccacgat gccatgccag gcttttctca ggagcttcaa tgagcgtcac ctacagacac 3319

aagcagggtga ctgcggtaac aacaggaatc atgtacaagc ctgctttctt ctcttggttt 3379

catttgggta atcagaagcc atttgagacc aagtgtgact gacttcatgg ttcacacctac 3439

tagccccctt ttttctcttc tttctcctta cctgtgggtg gattcttctc ggaaactgca 3499

aaatccaaga tgctggcact aggcgttatt cagtgggccc ttttgatgga catgtgacct 3559

gtagcccagt gccagagca tattatcata accacatttc aggggacgcc aacgtccatc 3619

cacctttgca tcgctacctg cagcgagcac agg 3652

<210> 6  
 <211> 923  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> misc\_feature  
 <222> (348)..(410)

&lt;223&gt; Signal Peptide

&lt;400&gt; 6

Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Thr Leu Ala Leu Ala Leu  
 1 5 10 15

Ala Leu Ala Gly Ala Phe Arg Ser Asp Lys Cys Gly Gly Thr Ile Lys  
 20 25 30

Ile Glu Asn Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr  
 35 40 45

His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Glu Pro Tyr  
 50 55 60

Gln Arg Ile Ile Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg  
 65 70 75 80

Asp Cys Lys Tyr Asp Tyr Val Glu Val Ile Asp Gly Glu Asn Glu Gly  
 85 90 95

Gly Arg Leu Trp Gly Lys Phe Cys Gly Lys Ile Ala Pro Ser Pro Val  
 100 105 110

Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu  
 115 120 125

Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly  
 130 135 140

Pro Glu Cys Ser Gln Asn Tyr Thr Ala Pro Thr Gly Val Ile Lys Ser  
 145 150 155 160

Pro Gly Phe Pro Glu Lys Tyr Pro Asn Cys Leu Glu Cys Thr Tyr Ile  
 165 170 175

Ile Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe  
 180 185 190

Asp Leu Glu Gln Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr  
 195 200 205

Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Glu Val Gly Pro His Ile  
 210 215 220

Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser  
 225 230 235 240

Gly Val Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu  
 245 250 255

Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Ile Ser Glu Asp  
 260 265 270

Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser  
 275 280 285

Asp Gln Ile Thr Ala Ser Ser Gln Tyr Gly Thr Asn Trp Ser Val Glu  
 290 295 300

Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp  
 305 310 315 320

Ser Tyr Lys Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val  
 325 330 335

Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys  
 340 345 350

Tyr Tyr Val Lys Thr Tyr Arg Val Asp Ile Ser Ser Asn Gly Glu Asp  
 355 360 365

Trp Ile Ser Leu Lys Glu Gly Asn Lys Ala Ile Ile Phe Gln Gly Asn  
 370 375 380

Thr Asn Pro Thr Asp Val Val Leu Gly Val Phe Ser Lys Pro Leu Ile  
 385 390 395 400

Thr Arg Phe Val Arg Ile Lys Pro Val Ser Trp Glu Thr Gly Ile Ser  
 405 410 415

Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser  
 420 425 430

Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr  
 435 440 445

Ala Ser Asn Gln Ala Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu  
 450 455 460

Val Thr Ser Arg Thr Gly Trp Ala Leu Pro Pro Ser Pro His Pro Tyr  
 465 470 475 480

Thr Asn Glu Trp Leu Gln Val Asp Leu Gly Asp Glu Lys Ile Val Arg  
 485 490 495

Gly Val Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met  
 500 505 510

Arg Lys Phe Lys Ile Ala Tyr Ser Asn Asn Gly Ser Asp Trp Lys Thr  
 515 520 525

Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn  
 530 535 540

Asn Tyr Asp Thr Pro Glu Leu Arg Thr Phe Ser Pro Leu Ser Thr Arg  
 545 550 555 560

Phe Ile Arg Ile Tyr Pro Glu Arg Ala Thr His Ser Gly Leu Gly Leu  
 565 570 575

Arg Met Glu Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro  
 580 585 590

Thr Thr Pro Asn Gly Asn Pro Val His Glu Cys Asp Asp Asp Gln Ala  
 595 600 605

Asn Cys His Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr  
 610 615 620

Thr Val Leu Ala Thr Glu Lys Pro Thr Ile Ile Asp Ser Thr Ile Gln  
 625 630 635 640

Ser Glu Phe Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser  
 645 650 655

His Lys Thr Phe Cys His Trp Glu His Asp Ser His Ala Gln Leu Arg  
 660 665 670

Trp Ser Val Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly  
 675 680 685

Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys  
 690 695 700

Val Ala Arg Leu Val Ser Pro Val Val Tyr Ser Gln Ser Ser Ala His  
 705 710 715 720

Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu  
 725 730 735

Arg Val Lys Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val  
 740 745 750

Trp Met Val Val Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val  
755 760 765

Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu  
770 775 780

Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile  
785 790 795 800

Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Thr Asp Leu Asp  
805 810 815

Lys Lys Asn Thr Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly  
820 825 830

Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly  
835 840 845

Asn Val Leu Lys Thr Leu Asp Pro Ile Leu Ile Thr Ile Ile Ala Met  
850 855 860

Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr  
865 870 875 880

Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu  
885 890 895

Glu Asn Tyr Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp  
900 905 910

Lys Leu Asn Pro Gln Ser Asn Tyr Ser Glu Ala  
915 920

<210> 7  
<211> 4769  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (567) .. (3347)

<400> 7  
aaactggagc tccaccgcgg tggcgccgc cggggcaggt ctagaattca gcggccgctg 60  
aattctatcc agcggtcggt gcctctgccc gcgtgtgtgt cccgggtgcc gggggacctg 120  
tgtcagttag cgcttctgag atcacacagc tgcttagggg ccgtgtgatg cccagggcaa 180  
ttcttggtt tgatttttat tattattact attattttgc gttcagcttt cgggaaaccc 240



tcgtgatgtt gtaggataaa ggaaatgaca ctttgaggaa ctggagagaa catacacgcg	300
tttgggtttg aagaggaaac cggctctccgc ttccttagct tgctccctct ttgctgattt	360
caagagctat ctcctatgag gtggagatat tccagcaaga ataaagggtga agacagactg	420
actgccagga cccaggagga aaacgttgat cgttagagac ctttgcagaa gacaccacca	480
ggaggaaaat tagagaggaa aaacacaaag acataattat aggagatccc acaaacctag	540
cccgaggagag agcctctctg tcaaaa atg gat atg ttt cct ctt acc tgg gtt	593
Met Asp Met Phe Pro Leu Thr Trp Val	
1 5	
ttc tta gct ctg tac ttt tca gga cac gaa gtg aga agc cag caa gat	641
Phe Leu Ala Leu Tyr Phe Ser Gly His Glu Val Arg Ser Gln Gln Asp	
10 15 20 25	
cca ccc tgc gga ggt cgg ccg aat tcc aaa gat gct ggc tac atc act	689
Pro Pro Cys Gly Gly Arg Pro Asn Ser Lys Asp Ala Gly Tyr Ile Thr	
30 35 40	
tcc cca ggc tac ccc cag gac tat ccc tcc cac cag aac tgt gag tgg	737
Ser Pro Gly Tyr Pro Gln Asp Tyr Pro Ser His Gln Asn Cys Glu Trp	
45 50 55	
att gtc tac gcc ccc gaa ccc aac cag aag att gtt ctc aac ttc aac	785
Ile Val Tyr Ala Pro Glu Pro Asn Gln Lys Ile Val Leu Asn Phe Asn	
60 65 70	
cct cac ttt gaa atc gag aaa cac gac tgc aag tat gac ttc att gag	833
Pro His Phe Glu Ile Glu Lys His Asp Cys Lys Tyr Asp Phe Ile Glu	
75 80 85	
att cgg gat ggg gac agt gag tca gct gac ctc ctg ggc aag cac tgt	881
Ile Arg Asp Gly Asp Ser Glu Ser Ala Asp Leu Leu Gly Lys His Cys	
90 95 100 105	
ggg aac atc gcc ccg ccc acc atc atc tcc tca ggc tcc gtg tta tac	929
Gly Asn Ile Ala Pro Pro Thr Ile Ile Ser Ser Gly Ser Val Leu Tyr	
110 115 120	
atc aag ttc acc tca gac tac gcc cgg cag ggg gca ggt ttc tct cta	977
Ile Lys Phe Thr Ser Asp Tyr Ala Arg Gln Gly Ala Gly Phe Ser Leu	
125 130 135	
cgc tat gag atc ttc aaa aca ggc tct gaa gat tgt tcc aag aac ttt	1025
Arg Tyr Glu Ile Phe Lys Thr Gly Ser Glu Asp Cys Ser Lys Asn Phe	
140 145 150	
aca agc ccc aat ggg acc att gaa tct cca ggg ttt cca gag aag tat	1073
Thr Ser Pro Asn Gly Thr Ile Glu Ser Pro Gly Phe Pro Glu Lys Tyr	
155 160 165	
cca cac aat ctg gac tgt acc ttc acc atc ctg gcc aaa ccc agg atg	1121
Pro His Asn Leu Asp Cys Thr Phe Thr Ile Leu Ala Lys Pro Arg Met	
170 175 180 185	
gag atc atc cta cag ttc ctg acc ttt gac ctg gag cat gac cct cta	1169
Glu Ile Ile Leu Gln Phe Leu Thr Phe Asp Leu Glu His Asp Pro Leu	
190 195 200	

caa gtg ggg gaa gga gac tgt aaa tat gac tgg ctg gac atc tgg gat Gln Val Gly Glu Gly Asp Cys Lys Tyr Asp Trp Leu Asp Ile Trp Asp 205 210 215	1217
ggc att cca cat gtt gga cct ctg att ggc aag tac tgt ggg acg aaa Gly Ile Pro His Val Gly Pro Leu Ile Gly Lys Tyr Cys Gly Thr Lys 220 225 230	1265
aca ccc tcc aaa ctc cgc tcg tcc acg ggg atc ctc tcc ttg acc ttt Thr Pro Ser Lys Leu Arg Ser Ser Thr Gly Ile Leu Ser Leu Thr Phe 235 240 245	1313
cac acg gac atg gca gtg gcc aag gat ggc ttc tcc gca cgt tac tat His Thr Asp Met Ala Val Ala Lys Asp Gly Phe Ser Ala Arg Tyr Tyr 250 255 260 265	1361
ttg atc cac cag gag cca cct gag aat ttt cag tgc aat gtc cct ttg Leu Ile His Gln Glu Pro Pro Glu Asn Phe Gln Cys Asn Val Pro Leu 270 275 280	1409
gga atg gag tct ggc cgg att gct aat gaa cag atc agt gcc tcc tcc Gly Met Glu Ser Gly Arg Ile Ala Asn Glu Gln Ile Ser Ala Ser Ser 285 290 295	1457
acc ttc tct gat ggg agg tgg act cct caa cag agc cgg ctc cat ggt Thr Phe Ser Asp Gly Arg Trp Thr Pro Gln Gln Ser Arg Leu His Gly 300 305 310	1505
gat gac aat ggc tgg aca ccc aat ttg gat tcc aac aag gag tat ctc Asp Asp Asn Gly Trp Thr Pro Asn Leu Asp Ser Asn Lys Glu Tyr Leu 315 320 325	1553
cag gtg gac ctg cgc ttc cta acc atg ctc aca gcc att gca aca cag Gln Val Asp Leu Arg Phe Leu Thr Met Leu Thr Ala Ile Ala Thr Gln 330 335 340 345	1601
gga gcc att tcc agg gaa acc cag aaa ggc tac tac gtc aaa tcg tac Gly Ala Ile Ser Arg Glu Thr Gln Lys Gly Tyr Tyr Val Lys Ser Tyr 350 355 360	1649
aag ctg gaa gtc agc aca aat ggt gaa gat tgg atg gtc tac cgg cat Lys Leu Glu Val Ser Thr Asn Gly Glu Asp Trp Met Val Tyr Arg His 365 370 375	1697
ggc aaa aac cac aag ata ttc caa gcg aac aat gat gcg acc gag gtg Gly Lys Asn His Lys Ile Phe Gln Ala Asn Asn Asp Ala Thr Glu Val 380 385 390	1745
gtg cta aac aag ctc cac atg cca ctg ctg act cgg ttc atc agg atc Val Leu Asn Lys Leu His Met Pro Leu Leu Thr Arg Phe Ile Arg Ile 395 400 405	1793
cgc ccg cag acg tgg cat ttg ggc att gcc ctt cgc ctg gag ctc ttt Arg Pro Gln Thr Trp His Leu Gly Ile Ala Leu Arg Leu Glu Leu Phe 410 415 420 425	1841
ggc tgc cgg gtc aca gat gca ccc tgc tcc aac atg ctg ggg atg ctc Gly Cys Arg Val Thr Asp Ala Pro Cys Ser Asn Met Leu Gly Met Leu 430 435 440	1889
tcg ggc ctc att gct gat acc cag atc tct gcc tcc tcc acc cga gag Ser Gly Leu Ile Ala Asp Thr Gln Ile Ser Ala Ser Ser Thr Arg Glu 445 450 455	1937

tac ctc tgg agc ccc agt gct gcc cgc ctg gtt agt agc cgc tct ggc Tyr Leu Trp Ser Pro Ser Ala Ala Arg Leu Val Ser Ser Arg Ser Gly 460 465 470	1985
tgg ttt cct cgg aac cct caa gcc cag cca ggt gaa gaa tgg ctt cag Trp Phe Pro Arg Asn Pro Gln Ala Gln Pro Gly Glu Glu Trp Leu Gln 475 480 485	2033.
gta gac ctg ggg aca ccc aag aca gtg aaa ggg gtc atc atc cag gga Val Asp Leu Gly Thr Pro Lys Thr Val Lys Gly Val Ile Ile Gln Gly 490 495 500 505	2081
gcc cga gga gga gac agc atc act gcc gtg gaa gcc agg gcg ttt gta Ala Arg Gly Gly Asp Ser Ile Thr Ala Val Glu Ala Arg Ala Phe Val 510 515 520	2129
cgc aag ttc aaa gtc tcc tac agc cta aat ggc aag gac tgg gaa tat Arg Lys Phe Lys Val Ser Tyr Ser Leu Asn Gly Lys Asp Trp Glu Tyr 525 530 535	2177
atc cag gac ccc agg act cag cag aca aag ctg ttt gaa ggg aac atg Ile Gln Asp Pro Arg Thr Gln Gln Thr Lys Leu Phe Glu Gly Asn Met 540 545 550	2225
cac tat gac acc cct gac atc cga agg ttc gat cct gtt cca gcg cag His Tyr Asp Thr Pro Asp Ile Arg Arg Phe Asp Pro Val Pro Ala Gln 555 560 565	2273
tat gtg cgg gtg tac cca gag agg tgg tgc cca gca ggc atc ggg atg Tyr Val Arg Val Tyr Pro Glu Arg Trp Ser Pro Ala Gly Ile Gly Met 570 575 580 585	2321
agg ctg gag gtg ctg ggc tgt gac tgg aca gac tca aag ccc aca gtg Arg Leu Glu Val Leu Gly Cys Asp Trp Thr Asp Ser Lys Pro Thr Val 590 595 600	2369
gag acg ctg gga ccc acc gtg aag agt gaa gag act acc acc cca tat Glu Thr Leu Gly Pro Thr Val Lys Ser Glu Glu Thr Thr Thr Pro Tyr 605 610 615	2417.
ccc atg gat gag gat gcc acc gag tgt ggg gaa aac tgc agc ttt gag Pro Met Asp Glu Asp Ala Thr Glu Cys Gly Glu Asn Cys Ser Phe Glu 620 625 630	2465.
gat gac aaa gat ttg caa ctt cct tca gga ttc aac tgc aac ttt gat Asp Asp Lys Asp Leu Gln Leu Pro Ser Gly Phe Asn Cys Asn Phe Asp 635 640 645	2513
ttt ccg gaa gag acc tgt ggt tgg gtg tac gac cat gcc aag tgg ctc Phe Pro Glu Glu Thr Cys Gly Trp Val Tyr Asp His Ala Lys Trp Leu 650 655 660 665	2561
cgg agc acg tgg atc agc agc gct aac ccc aat gac aga aca ttt cca Arg Ser Thr Trp Ile Ser Ser Ala Asn Pro Asn Asp Arg Thr Phe Pro 670 675 680	2609
gat gac aag aac ttc ttg aaa ctg cag agt gat ggc cga cga gag ggc Asp Asp Lys Asn Phe Leu Lys Leu Gln Ser Asp Gly Arg Arg Glu Gly 685 690 695	2657
cag tac ggg cgg ctc atc agc cca ccg gtg cac ctg ccc cga agc cct Gln Tyr Gly Arg Leu Ile Ser Pro Pro Val His Leu Pro Arg Ser Pro 700 705 710	2705

gtg tgc atg gag ttc cag tac caa gcc atg ggc ggc cac ggg gtg gca 2753  
Val Cys Met Glu Phe Gln Tyr Gln Ala Met Gly Gly His Gly Val Ala  
715 720 725

ctg cag gtg gtt cgg gaa gcc agc cag gaa agc aaa ctc ctt tgg gtc 2801  
Leu Gln Val Val Arg Glu Ala Ser Gln Glu Ser Lys Leu Leu Trp Val  
730 735 740 745

atc cgt gag gac cag ggc agc gag tgg aag cac ggg cgc att atc ctg 2849  
Ile Arg Glu Asp Gln Gly Ser Glu Trp Lys His Gly Arg Ile Ile Leu  
750 755 760

ccc agc tat gac atg gag tat cag atc gtg ttc gag gga gtg ata ggg 2897  
Pro Ser Tyr Asp Met Glu Tyr Gln Ile Val Phe Glu Gly Val Ile Gly  
765 770 775

aag gga cga tcg gga gag att tcc ggc gat gac att cgg ata agc act 2945  
Lys Gly Arg Ser Gly Glu Ile Ser Gly Asp Asp Ile Arg Ile Ser Thr  
780 785 790

gat gtc cca ctg gag aac tgc atg gaa ccc ata tca gct ttt gca gtg 2993  
Asp Val Pro Leu Glu Asn Cys Met Glu Pro Ile Ser Ala Phe Ala Val  
795 800 805

gac atc cca gaa acc cat ggg gga gag ggc tat gaa gat gag att gat 3041  
Asp Ile Pro Glu Thr His Gly Gly Glu Gly Tyr Glu Asp Glu Ile Asp  
810 815 820 825

gat gaa tat gaa gga gat tgg agc aac tct tct tcc tct acc tca ggg 3089  
Asp Glu Tyr Glu Gly Asp Trp Ser Asn Ser Ser Ser Ser Thr Ser Gly  
830 835 840

gct ggt gac ccc tca tct ggc aaa gaa aag agc tgg ctg tac acc cta 3137  
Ala Gly Asp Pro Ser Ser Gly Lys Glu Lys Ser Trp Leu Tyr Thr Leu  
845 850 855

gat ccc att ctg atc acc atc atc gcc atg agc tcg ctg ggg gtc ctg 3185  
Asp Pro Ile Leu Ile Thr Ile Ile Ala Met Ser Ser Leu Gly Val Leu  
860 865 870

ctg ggg gcc acc tgt gcg ggc ctc ctc ctt tac tgc acc tgc tcc tat 3233  
Leu Gly Ala Thr Cys Ala Gly Leu Leu Leu Tyr Cys Thr Cys Ser Tyr  
875 880 885

tcg ggt ctg agt tcg agg agc tgc acc aca ctg gag aac tac aac ttt 3281  
Ser Gly Leu Ser Ser Arg Ser Cys Thr Thr Leu Glu Asn Tyr Asn Phe  
890 895 900 905

gag ctc tac gat ggc ctc aag cac aag gtc aag atc aat cat cag aag 3329  
Glu Leu Tyr Asp Gly Leu Lys His Lys Val Lys Ile Asn His Gln Lys  
910 915 920

tgc tgc tcg gag gca tga ccgattgtgt ctggatcgct tctggcgttt 3377  
Cys Cys Ser Glu Ala  
925

cattccagtg agaggggcta gcgaagatta cagttttgtt ttgttttgtt ttgttttccc 3437

tttggaact gaatgccata atctggatca aagtgttcca gaatactgaa ggtatggaca 3497

ggacagacag gccagtctag ggagaaaggg agatgcagct gtgaaggggga tcgttgccca 3557

ccaggactgt ggtggccaag tgaatgcagg aaccggggccc ggaattccgg ctctcggcta 3617

```

aaatctcagc tgcctctgga aaggctcaac cataactcagt gccaaactcag actctgttgc 3677
tgtgggtgtca acatggatgg atcatctgtgta ccttgtatatt ttagcagaat tcatgctcag 3737
atttcttttgt tctgaatcct tgctttgtgc tagacacaaa gcatacatgt ccttctaaaa 3797
ttaatatgat cactataatc tcctgtgtgc agaattcaga aatagacctt tgaaaccatt 3857
tgcatgtgtga gtgcagatcc atgactgggg ctagtgcagc aatgaaacag aattccagaa 3917
acagtgtgtt ctttttatta tgggaaaata cagataaaaa tggccactga tgaacatgaa 3977
agttagcact ttcccaacac agtgtacact tgcaaccttg ttttggattt ctcatacacc 4037
aagactgtga aacacaaaatt tcaagaatgt gttcaaatgt gtgtgtgtgt gtgtgtgtgt 4097
gtgtgtgtgt gtgtgtatgt gtgtgtgtgt gtgtgtgctt gtgtgtttct gtcagtggta 4157
tgagtgatat gtatgcatgt gtgtatgtat atgtatgtat gtatgtatgt atgtacgtac 4217
atatgtatgt atgtatgtat gtatgtatgt atgtatatgt gtgtgtgtgt ttgtgtgtgt 4277
gtgtgtttgt gtgtgtgtgt gtggtaagtg tggtagtgtgt gtatgcattt gtctatatgt 4337
gtatctgtgt gtctatgtgt ttctgtcagt ggaatgagtg gcatgtgtgc atgtgtatgt 4397
atgtggatat gtgtgttgtgt tttatgtgct tgtgtataag aggtaagtgt ggtgtgtgtg 4457
catgtgtctc tgtgtgtgtt tgtctgtgta cctctttgta taagtacctg tgtttgtatg 4517
tgggaatatg tatattgagg cattgctgtg ttagtatgtt tatagaaaag aagacagtct 4577
gagatgtctt cctcaatacc tctccactta tatcttggat agacaaaagt aatgacaaaa 4637
aattgctggg gtgtatatgg aaaaggggga cacatatcca tggatggtag aagtgtaaac 4697
tgtgcagtca ctgtggacat caatatgcag gttcttcaca aatgtagata taaagctact 4757
atagttatac cc 4769

```

&lt;210&gt; 8

&lt;211&gt; 926

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 8

```

Met Asp Met Phe Pro Leu Thr Trp Val Phe Leu Ala Leu Tyr Phe Ser
1           5           10          15

```

```

Gly His Glu Val Arg Ser Gln Gln Asp Pro Pro Cys Gly Gly Arg Pro
          20           25           30

```

```

Asn Ser Lys Asp Ala Gly Tyr Ile Thr Ser Pro Gly Tyr Pro Gln Asp
          35           40           45

```

```

Tyr Pro Ser His Gln Asn Cys Glu Trp Ile Val Tyr Ala Pro Glu Pro
          50           55           60

```

Asn Gln Lys Ile Val Leu Asn Phe Asn Pro His Phe Glu Ile Glu Lys  
 65 70 75 80

His Asp Cys Lys Tyr Asp Phe Ile Glu Ile Arg Asp Gly Asp Ser Glu  
 85 90 95

Ser Ala Asp Leu Leu Gly Lys His Cys Gly Asn Ile Ala Pro Pro Thr  
 100 105 110

Ile Ile Ser Ser Gly Ser Val Leu Tyr Ile Lys Phe Thr Ser Asp Tyr  
 115 120 125

Ala Arg Gln Gly Ala Gly Phe Ser Leu Arg Tyr Glu Ile Phe Lys Thr  
 130 135 140

Gly Ser Glu Asp Cys Ser Lys Asn Phe Thr Ser Pro Asn Gly Thr Ile  
 145 150 155 160

Glu Ser Pro Gly Phe Pro Glu Lys Tyr Pro His Asn Leu Asp Cys Thr  
 165 170 175

Phe Thr Ile Leu Ala Lys Pro Arg Met Glu Ile Ile Leu Gln Phe Leu  
 180 185 190

Thr Phe Asp Leu Glu His Asp Pro Leu Gln Val Gly Glu Gly Asp Cys  
 195 200 205

Lys Tyr Asp Trp Leu Asp Ile Trp Asp Gly Ile Pro His Val Gly Pro  
 210 215 220

Leu Ile Gly Lys Tyr Cys Gly Thr Lys Thr Pro Ser Lys Leu Arg Ser  
 225 230 235 240

Ser Thr Gly Ile Leu Ser Leu Thr Phe His Thr Asp Met Ala Val Ala  
 245 250 255

Lys Asp Gly Phe Ser Ala Arg Tyr Tyr Leu Ile His Gln Glu Pro Pro  
 260 265 270

Glu Asn Phe Gln Cys Asn Val Pro Leu Gly Met Glu Ser Gly Arg Ile  
 275 280 285

Ala Asn Glu Gln Ile Ser Ala Ser Ser Thr Phe Ser Asp Gly Arg Trp  
 290 295 300

Thr Pro Gln Gln Ser Arg Leu His Gly Asp Asp Asn Gly Trp Thr Pro  
 305 310 315 320

Asn Leu Asp Ser Asn Lys Glu Tyr Leu Gln Val Asp Leu Arg Phe Leu  
 325 330 335

Thr Met Leu Thr Ala Ile Ala Thr Gln Gly Ala Ile Ser Arg Glu Thr  
 340 345 350

Gln Lys Gly Tyr Tyr Val Lys Ser Tyr Lys Leu Glu Val Ser Thr Asn  
 355 360 365

Gly Glu Asp Trp Met Val Tyr Arg His Gly Lys Asn His Lys Ile Phe  
 370 375 380

Gln Ala Asn Asn Asp Ala Thr Glu Val Val Leu Asn Lys Leu His Met  
 385 390 395 400

Pro Leu Leu Thr Arg Phe Ile Arg Ile Arg Pro Gln Thr Trp His Leu  
 405 410 415

Gly Ile Ala Leu Arg Leu Glu Leu Phe Gly Cys Arg Val Thr Asp Ala  
 420 425 430

Pro Cys Ser Asn Met Leu Gly Met Leu Ser Gly Leu Ile Ala Asp Thr  
 435 440 445

Gln Ile Ser Ala Ser Ser Thr Arg Glu Tyr Leu Trp Ser Pro Ser Ala  
 450 455 460

Ala Arg Leu Val Ser Ser Arg Ser Gly Trp Phe Pro Arg Asn Pro Gln  
 465 470 475 480

Ala Gln Pro Gly Glu Glu Trp Leu Gln Val Asp Leu Gly Thr Pro Lys  
 485 490 495

Thr Val Lys Gly Val Ile Ile Gln Gly Ala Arg Gly Gly Asp Ser Ile  
 500 505 510

Thr Ala Val Glu Ala Arg Ala Phe Val Arg Lys Phe Lys Val Ser Tyr  
 515 520 525

Ser Leu Asn Gly Lys Asp Trp Glu Tyr Ile Gln Asp Pro Arg Thr Gln  
 530 535 540

Gln Thr Lys Leu Phe Glu Gly Asn Met His Tyr Asp Thr Pro Asp Ile  
 545 550 555 560

Arg Arg Phe Asp Pro Val Pro Ala Gln Tyr Val Arg Val Tyr Pro Glu  
 565 570 575

Arg Trp Ser Pro Ala Gly Ile Gly Met Arg Leu Glu Val Leu Gly Cys  
 580 585 590

Asp Trp Thr Asp Ser Lys Pro Thr Val Glu Thr Leu Gly Pro Thr Val  
 595 600 605

Lys Ser Glu Glu Thr Thr Thr Pro Tyr Pro Met Asp Glu Asp Ala Thr  
 610 615 620

Glu Cys Gly Glu Asn Cys Ser Phe Glu Asp Asp Lys Asp Leu Gln Leu  
 625 630 635 640

Pro Ser Gly Phe Asn Cys Asn Phe Asp Phe Pro Glu Glu Thr Cys Gly  
 645 650 655

Trp Val Tyr Asp His Ala Lys Trp Leu Arg Ser Thr Trp Ile Ser Ser  
 660 665 670

Ala Asn Pro Asn Asp Arg Thr Phe Pro Asp Asp Lys Asn Phe Leu Lys  
 675 680 685

Leu Gln Ser Asp Gly Arg Arg Glu Gly Gln Tyr Gly Arg Leu Ile Ser  
 690 695 700

Pro Pro Val His Leu Pro Arg Ser Pro Val Cys Met Glu Phe Gln Tyr  
 705 710 715 720

Gln Ala Met Gly Gly His Gly Val Ala Leu Gln Val Val Arg Glu Ala  
 725 730 735

Ser Gln Glu Ser Lys Leu Leu Trp Val Ile Arg Glu Asp Gln Gly Ser  
 740 745 750

Glu Trp Lys His Gly Arg Ile Ile Leu Pro Ser Tyr Asp Met Glu Tyr  
 755 760 765

Gln Ile Val Phe Glu Gly Val Ile Gly Lys Gly Arg Ser Gly Glu Ile  
 770 775 780

Ser Gly Asp Asp Ile Arg Ile Ser Thr Asp Val Pro Leu Glu Asn Cys  
 785 790 795 800

Met Glu Pro Ile Ser Ala Phe Ala Val Asp Ile Pro Glu Thr His Gly  
 805 810 815

Gly Glu Gly Tyr Glu Asp Glu Ile Asp Asp Glu Tyr Glu Gly Asp Trp  
 820 825 830



Ser Asn Ser Ser Ser Ser Thr Ser Gly Ala Gly Asp Pro Ser Ser Gly  
835 840 845

Lys Glu Lys Ser Trp Leu Tyr Thr Leu Asp Pro Ile Leu Ile Thr Ile  
850 855 860

Ile Ala Met Ser Ser Leu Gly Val Leu Leu Gly Ala Thr Cys Ala Gly  
865 870 875 880

Leu Leu Leu Tyr Cys Thr Cys Ser Tyr Ser Gly Leu Ser Ser Arg Ser  
885 890 895

Cys Thr Thr Leu Glu Asn Tyr Asn Phe Glu Leu Tyr Asp Gly Leu Lys  
900 905 910

His Lys Val Lys Ile Asn His Gln Lys Cys Cys Ser Glu Ala  
915 920 925

<210> 9

<211> 2530

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (16)..(2331)

<400> 9

ggaattccct gcagc atg ggc tgg tta act agg att gtc tgt ctt ttc tgg 51  
Met Gly Trp Leu Thr Arg Ile Val Cys Leu Phe Trp  
1 5 10

gga gta tta ctt aca gca aga gca aac tat cag aat ggg aag aac aat 99  
Gly Val Leu Leu Thr Ala Arg Ala Asn Tyr Gln Asn Gly Lys Asn Asn  
15 20 25

gtg cca agg ctg aaa tta tcc tac aaa gaa atg ttg gaa tcc aac aat 147  
Val Pro Arg Leu Lys Leu Ser Tyr Lys Glu Met Leu Glu Ser Asn Asn  
30 35 40

gtg atc act ttc aat ggc ttg gcc aac agc tcc agt tat cat acc ttc 195  
Val Ile Thr Phe Asn Gly Leu Ala Asn Ser Ser Ser Tyr His Thr Phe  
45 50 55 60

ctt ttg gat gag gaa cgg agt agg ctg tat gtt gga gca aag gat cac 243  
Leu Leu Asp Glu Glu Arg Ser Arg Leu Tyr Val Gly Ala Lys Asp His  
65 70 75

ata ttt tca ttc gac ctg gtt aat atc aag gat ttt caa aag att gtg 291  
Ile Phe Ser Phe Asp Leu Val Asn Ile Lys Asp Phe Gln Lys Ile Val  
80 85 90

tgg cca gta tct tac acc aga aga gat gaa tgc aag tgg gct gga aaa 339  
Trp Pro Val Ser Tyr Thr Arg Arg Asp Glu Cys Lys Trp Ala Gly Lys  
95 100 105

gac atc ctg aaa gaa tgt gct aat ttc atc aag gta ctt aag gca tat Asp Ile Leu Lys Glu Cys Ala Asn Phe Ile Lys Val Leu Lys Ala Tyr 110 115 120	387
aat cag act cac ttg tac gcc tgt gga acg ggg gct ttt cat cca att Asn Gln Thr His Leu Tyr Ala Cys Gly Thr Gly Ala Phe His Pro Ile 125 130 135 140	435
tgc acc tac att gaa att gga cat cat cct gag gac aat att ttt aag Cys Thr Tyr Ile Glu Ile Gly His His Pro Glu Asp Asn Ile Phe Lys 145 150 155	483
ctg gag aac tca cat ttt gaa aac ggc cgt ggg aag agt cca tat gac Leu Glu Asn Ser His Phe Glu Asn Gly Arg Gly Lys Ser Pro Tyr Asp 160 165 170	531
cct aag ctg ctg aca gca tcc ctt tta ata gat gga gaa tta tac tct Pro Lys Leu Leu Thr Ala Ser Leu Leu Ile Asp Gly Glu Leu Tyr Ser 175 180 185	579
gga act gca gct gat ttt atg ggg cga gac ttt gct atc ttc cga act Gly Thr Ala Ala Asp Phe Met Gly Arg Asp Phe Ala Ile Phe Arg Thr 190 195 200	627
ctt ggg cac cac cac cca atc agg aca gag cag cat gat tcc agg tgg Leu Gly His His His Pro Ile Arg Thr Glu Gln His Asp Ser Arg Trp 205 210 215 220	675
ctc aat gat cca aag ttc att agt gcc cac ctc atc tca gag agt gac Leu Asn Asp Pro Lys Phe Ile Ser Ala His Leu Ile Ser Glu Ser Asp 225 230 235	723
aat cct gaa gat gac aaa gta tac ttt ttc ttc cgt gaa aat gca ata Asn Pro Glu Asp Asp Lys Val Tyr Phe Phe Phe Arg Glu Asn Ala Ile 240 245 250	771
gat gga gaa cac tct gga aaa gct act cac gct aga ata ggt cag ata Asp Gly Glu His Ser Gly Lys Ala Thr His Ala Arg Ile Gly Gln Ile 255 260 265	819
tgc aag aat gac ttt gga ggg cac aga agt ctg gtg aat aaa tgg aca Cys Lys Asn Asp Phe Gly Gly His Arg Ser Leu Val Asn Lys Trp Thr 270 275 280	867
aca ttc ctc aaa gct cgt ctg att tgc tca gtg cca ggt cca aat ggc Thr Phe Leu Lys Ala Arg Leu Ile Cys Ser Val Pro Gly Pro Asn Gly 285 290 295 300	915
att gac act cat ttt gat gaa ctg cag gat gta ttc cta atg aac ttt Ile Asp Thr His Phe Asp Glu Leu Gln Asp Val Phe Leu Met Asn Phe 305 310 315	963
aaa gat cct aaa aat cca gtt gta tat gga gtg ttt acg act tcc agt Lys Asp Pro Lys Asn Pro Val Val Tyr Gly Val Phe Thr Thr Ser Ser 320 325 330	1011
aac att ttc aag gga tca gcc gtg tgt atg tat agc atg agt gat gtg Asn Ile Phe Lys Gly Ser Ala Val Cys Met Tyr Ser Met Ser Asp Val 335 340 345	1059
aga agg gtg ttc ctt ggt cca tat gcc cac agg gat gga ccc aac tat Arg Arg Val Phe Leu Gly Pro Tyr Ala His Arg Asp Gly Pro Asn Tyr 350 355 360	1107

caa tgg gtg cct tat caa gga aga gtc ccc tat cca cgg cca gga act	1155
Gln Trp Val Pro Tyr Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Thr	
365 370 375 380	
tgt ccc agc aaa aca ttt ggt ggt ttt gac tct aca aag gac ctt cct	1203
Cys Pro Ser Lys Thr Phe Gly Gly Phe Asp Ser Thr Lys Asp Leu Pro	
385 390 395	
gat gat gtt ata acc ttt gca aga agt cat cca gcc atg tac aat cca	1251
Asp Asp Val Ile Thr Phe Ala Arg Ser His Pro Ala Met Tyr Asn Pro	
400 405 410	
gtg ttt cct atg aac aat cgc cca ata gtg atc aaa acg gat gta aat	1299
Val Phe Pro Met Asn Asn Arg Pro Ile Val Ile Lys Thr Asp Val Asn	
415 420 425	
tat caa ttt aca caa att gtc gta gac cga gtg gat gca gaa gat gga	1347
Tyr Gln Phe Thr Gln Ile Val Val Asp Arg Val Asp Ala Glu Asp Gly	
430 435 440	
cag tat gat gtt atg ttt atc gga aca gat gtt ggg acc gtt ctt aaa	1395
Gln Tyr Asp Val Met Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys	
445 450 455 460	
gta gtt tca att cct aag gag act tgg tat gat tta gaa gag gtt ctg	1443
Val Val Ser Ile Pro Lys Glu Thr Trp Tyr Asp Leu Glu Glu Val Leu	
465 470 475	
ctg gaa gaa atg aca gtt ttt cgg gaa ccg act gct att tca gca atg	1491
Leu Glu Glu Met Thr Val Phe Arg Glu Pro Thr Ala Ile Ser Ala Met	
480 485 490	
gag ctt tcc act aag cag caa caa cta tat att ggt tca acg gct ggg	1539
Glu Leu Ser Thr Lys Gln Gln Gln Leu Tyr Ile Gly Ser Thr Ala Gly	
495 500 505	
gtt gcc cag ctc cct tta cac cgg tgt gat att tac ggg aaa gcg tgt	1587
Val Ala Gln Leu Pro Leu His Arg Cys Asp Ile Tyr Gly Lys Ala Cys	
510 515 520	
gct gag tgt tgc ctc gcc cga gac cct tac tgt gct tgg gat ggt tct	1635
Ala Glu Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ser	
525 530 535 540	
gca tgt tct cgc tat ttt ccc act gca aag aga cgc aca aga cga caa	1683
Ala Cys Ser Arg Tyr Phe Pro Thr Ala Lys Arg Arg Thr Arg Arg Gln	
545 550 555	
gat ata aga aat gga gac cca ctg act cac tgt tca gac tta cac cat	1731
Asp Ile Arg Asn Gly Asp Pro Leu Thr His Cys Ser Asp Leu His His	
560 565 570	
gat aat cac cat ggc cac agc cct gaa gag aga atc atc tat ggt gta	1779
Asp Asn His His Gly His Ser Pro Glu Glu Arg Ile Ile Tyr Gly Val	
575 580 585	
gag aat agt agc aca ttt ttg gaa tgc agt ccg aag tcg cag aga gcg	1827
Glu Asn Ser Ser Thr Phe Leu Glu Cys Ser Pro Lys Ser Gln Arg Ala	
590 595 600	
ctg gtc tat tgg caa ttc cag agg cga aat gaa gag cga aaa gaa gag	1875
Leu Val Tyr Trp Gln Phe Gln Arg Arg Asn Glu Glu Arg Lys Glu Glu	
605 610 615 620	

atc aga gtg gat gat cat atc atc agg aca gat caa ggc ctt ctg cta 1923  
 Ile Arg Val Asp Asp His Ile Ile Arg Thr Asp Gln Gly Leu Leu Leu  
 625 630 635

cgt agt cta caa cag aag gat tca ggc aat tac ctc tgc cat gcg gtg 1971  
 Arg Ser Leu Gln Gln Lys Asp Ser Gly Asn Tyr Leu Cys His Ala Val  
 640 645 650

gaa cat ggg ttc ata caa act ctt ctt aag gta acc ctg gaa gtc att 2019  
 Glu His Gly Phe Ile Gln Thr Leu Leu Lys Val Thr Leu Glu Val Ile  
 655 660 665

gac aca gag cat ttg gaa gaa ctt ctt cat aaa gat gat gat gga gat 2067  
 Asp Thr Glu His Leu Glu Glu Leu Leu His Lys Asp Asp Asp Gly Asp  
 670 675 680

ggc tct aag acc aaa gaa atg tcc aat agc atg aca cct agc cag aag 2115  
 Gly Ser Lys Thr Lys Glu Met Ser Asn Ser Met Thr Pro Ser Gln Lys  
 685 690 695 700

gtc tgg tac aga gac ttc atg cag ctc atc aac cac ccc aat ctc aac 2163  
 Val Trp Tyr Arg Asp Phe Met Gln Leu Ile Asn His Pro Asn Leu Asn  
 705 710 715

acg atg gat gag ttc tgt gaa caa gtt tgg aaa agg gac cga aaa caa 2211  
 Thr Met Asp Glu Phe Cys Glu Gln Val Trp Lys Arg Asp Arg Lys Gln  
 720 725 730

cgt cgg caa agg cca gga cat acc cca ggg aac agt aac aaa tgg aag 2259  
 Arg Arg Gln Arg Pro Gly His Thr Pro Gly Asn Ser Asn Lys Trp Lys  
 735 740 745

cac tta caa gaa aat aag aaa ggt aga aac agg agg acc cac gaa ttt 2307  
 His Leu Gln Glu Asn Lys Lys Gly Arg Asn Arg Arg Thr His Glu Phe  
 750 755 760

gag agg gca ccc agg agt gtc tga gctgcattac ctctagaaac ctcaaacaag 2361  
 Glu Arg Ala Pro Arg Ser Val  
 765 770

tagaaacttg cctagacaat aactggaaaa acaaatgcaa tatacatgaa cttttttcat 2421

ggcattatgt ggatgtttac aatggtggga aattcagctg agttccacca attataaatt 2481

aatccatga gtaactttcc taataggett ttttttcta ataccaccg 2530

<210> 10  
 <211> 771  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Met Gly Trp Leu Thr Arg Ile Val Cys Leu Phe Trp Gly Val Leu Leu  
 1 5 10 15

Thr Ala Arg Ala Asn Tyr Gln Asn Gly Lys Asn Asn Val Pro Arg Leu  
 20 25 30

Lys Leu Ser Tyr Lys Glu Met Leu Glu Ser Asn Asn Val Ile Thr Phe  
 35 40 45

Asn Gly Leu Ala Asn Ser Ser Ser Tyr His Thr Phe Leu Leu Asp Glu  
 50 55 60

Glu Arg Ser Arg Leu Tyr Val Gly Ala Lys Asp His Ile Phe Ser Phe  
 65 70 75 80

Asp Leu Val Asn Ile Lys Asp Phe Gln Lys Ile Val Trp Pro Val Ser  
 85 90 95

Tyr Thr Arg Arg Asp Glu Cys Lys Trp Ala Gly Lys Asp Ile Leu Lys  
 100 105 110

Glu Cys Ala Asn Phe Ile Lys Val Leu Lys Ala Tyr Asn Gln Thr His  
 115 120 125

Leu Tyr Ala Cys Gly Thr Gly Ala Phe His Pro Ile Cys Thr Tyr Ile  
 130 135 140

Glu Ile Gly His His Pro Glu Asp Asn Ile Phe Lys Leu Glu Asn Ser  
 145 150 155 160

His Phe Glu Asn Gly Arg Gly Lys Ser Pro Tyr Asp Pro Lys Leu Leu  
 165 170 175

Thr Ala Ser Leu Leu Ile Asp Gly Glu Leu Tyr Ser Gly Thr Ala Ala  
 180 185 190

Asp Phe Met Gly Arg Asp Phe Ala Ile Phe Arg Thr Leu Gly His His  
 195 200 205

His Pro Ile Arg Thr Glu Gln His Asp Ser Arg Trp Leu Asn Asp Pro  
 210 215 220

Lys Phe Ile Ser Ala His Leu Ile Ser Glu Ser Asp Asn Pro Glu Asp  
 225 230 235 240

Asp Lys Val Tyr Phe Phe Phe Arg Glu Asn Ala Ile Asp Gly Glu His  
 245 250 255

Ser Gly Lys Ala Thr His Ala Arg Ile Gly Gln Ile Cys Lys Asn Asp  
 260 265 270

Phe Gly Gly His Arg Ser Leu Val Asn Lys Trp Thr Thr Phe Leu Lys  
 275 280 285

Ala Arg Leu Ile Cys Ser Val Pro Gly Pro Asn Gly Ile Asp Thr His  
 290 295 300

Phe Asp Glu Leu Gln Asp Val Phe Leu Met Asn Phe Lys Asp Pro Lys  
 305 310 315 320

Asn Pro Val Val Tyr Gly Val Phe Thr Thr Ser Ser Asn Ile Phe Lys  
 325 330 335

Gly Ser Ala Val Cys Met Tyr Ser Met Ser Asp Val Arg Arg Val Phe  
 340 345 350

Leu Gly Pro Tyr Ala His Arg Asp Gly Pro Asn Tyr Gln Trp Val Pro  
 355 360 365

Tyr Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys  
 370 375 380

Thr Phe Gly Gly Phe Asp Ser Thr Lys Asp Leu Pro Asp Asp Val Ile  
 385 390 395 400

Thr Phe Ala Arg Ser His Pro Ala Met Tyr Asn Pro Val Phe Pro Met  
 405 410 415

Asn Asn Arg Pro Ile Val Ile Lys Thr Asp Val Asn Tyr Gln Phe Thr  
 420 425 430

Gln Ile Val Val Asp Arg Val Asp Ala Glu Asp Gly Gln Tyr Asp Val  
 435 440 445

Met Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys Val Val Ser Ile  
 450 455 460

Pro Lys Glu Thr Trp Tyr Asp Leu Glu Glu Val Leu Leu Glu Glu Met  
 465 470 475 480

Thr Val Phe Arg Glu Pro Thr Ala Ile Ser Ala Met Glu Leu Ser Thr  
 485 490 495

Lys Gln Gln Gln Leu Tyr Ile Gly Ser Thr Ala Gly Val Ala Gln Leu  
 500 505 510

Pro Leu His Arg Cys Asp Ile Tyr Gly Lys Ala Cys Ala Glu Cys Cys  
 515 520 525

Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ser Ala Cys Ser Arg  
 530 535 540

Tyr Phe Pro Thr Ala Lys Arg Arg Thr Arg Arg Gln Asp Ile Arg Asn  
 545 550 555 560

Gly Asp Pro Leu Thr His Cys Ser Asp Leu His His Asp Asn His His  
 565 570 575

Gly His Ser Pro Glu Glu Arg Ile Ile Tyr Gly Val Glu Asn Ser Ser  
 580 585 590

Thr Phe Leu Glu Cys Ser Pro Lys Ser Gln Arg Ala Leu Val Tyr Trp  
 595 600 605

Gln Phe Gln Arg Arg Asn Glu Glu Arg Lys Glu Glu Ile Arg Val Asp  
 610 615 620

Asp His Ile Ile Arg Thr Asp Gln Gly Leu Leu Leu Arg Ser Leu Gln  
 625 630 635 640

Gln Lys Asp Ser Gly Asn Tyr Leu Cys His Ala Val Glu His Gly Phe  
 645 650 655

Ile Gln Thr Leu Leu Lys Val Thr Leu Glu Val Ile Asp Thr Glu His  
 660 665 670

Leu Glu Glu Leu Leu His Lys Asp Asp Asp Gly Asp Gly Ser Lys Thr  
 675 680 685

Lys Glu Met Ser Asn Ser Met Thr Pro Ser Gln Lys Val Trp Tyr Arg  
 690 695 700

Asp Phe Met Gln Leu Ile Asn His Pro Asn Leu Asn Thr Met Asp Glu  
 705 710 715 720

Phe Cys Glu Gln Val Trp Lys Arg Asp Arg Lys Gln Arg Arg Gln Arg  
 725 730 735

Pro Gly His Thr Pro Gly Asn Ser Asn Lys Trp Lys His Leu Gln Glu  
 740 745 750

Asn Lys Lys Gly Arg Asn Arg Arg Thr His Glu Phe Glu Arg Ala Pro  
 755 760 765

Arg Ser Val  
 770

<210> 11  
 <211> 2919  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (236) .. (2485)

<400> 11  
 tctgtgattg tggccaggcg gggcaccctc ggaggggagg gttcggaagt ggaatgcgac 60  
 cccccagcct ctttccccta ggggctgtaa tctgatccct ggggactccc cccctagcct 120  
 cccgccctcg ccctcactgc tgactcctct tccagatcct ggggcagagt ccagggcagc 180  
 tcaaggctcc tccacacaca caccgctga accctgagca ccctgagctg ctgag atg 238  
 Met  
 1  
 ggg cgg gcc ggg gct gcc gcc gtg atc ccg ggc ctg gcc ctg ctc tgg 286  
 Gly Arg Ala Gly Ala Ala Ala Val Ile Pro Gly Leu Ala Leu Leu Trp  
 5 10 15  
 gca gtg ggg ctg ggg agt gcc gcc ccc agc ccc cca cgc ctt cgg ctc 334  
 Ala Val Gly Leu Gly Ser Ala Ala Pro Ser Pro Pro Arg Leu Arg Leu  
 20 25 30  
 tcc ttc caa gag ctc cag gcc tgg cat ggt ctc cag act ttc agc ctg 382  
 Ser Phe Gln Glu Leu Gln Ala Trp His Gly Leu Gln Thr Phe Ser Leu  
 35 40 45  
 gag cga acc tgc tgc tac cag gcc ttg ctg gtg gat gag gag cgt gga 430  
 Glu Arg Thr Cys Cys Tyr Gln Ala Leu Leu Val Asp Glu Glu Arg Gly  
 50 55 60 65  
 cgc ctg ttt gtg ggt gcc gag aac cat gtg gcc tcc ctc aac ctg gac 478  
 Arg Leu Phe Val Gly Ala Glu Asn His Val Ala Ser Leu Asn Leu Asp  
 70 75 80  
 aac atc agc aag cgg gcc aag aag ctg gcc tgg ccg gcc cct gtg gaa 526  
 Asn Ile Ser Lys Arg Ala Lys Lys Leu Ala Trp Pro Ala Pro Val Glu  
 85 90 95  
 tgg cga gag gag tgc aac tgg gca ggg aag gac att ggt act gag tgc 574  
 Trp Arg Glu Glu Cys Asn Trp Ala Gly Lys Asp Ile Gly Thr Glu Cys  
 100 105 110  
 atg aac ttc gtg aag ttg ctg cat gcc tac aac cgc acc cat ttg ctg 622  
 Met Asn Phe Val Lys Leu Leu His Ala Tyr Asn Arg Thr His Leu Leu  
 115 120 125  
 gcc tgt ggc acg gga gcc ttc cac cca acc tgt gcc ttt gtg gaa gtg 670  
 Ala Cys Gly Thr Gly Ala Phe His Pro Thr Cys Ala Phe Val Glu Val  
 130 135 140 145  
 ggc cac cgg gca gag gag ccc gtc ctc cgg ctg gac cca gga agg ata 718  
 Gly His Arg Ala Glu Glu Pro Val Leu Arg Leu Asp Pro Gly Arg Ile  
 150 155 160  
 gag gat ggc aag ggg aag agt cct tat gac ccc agg cat cgg gct gcc 766  
 Glu Asp Gly Lys Gly Lys Ser Pro Tyr Asp Pro Arg His Arg Ala Ala  
 165 170 175



tcc gtg ctg gtg ggg gag gag cta tac tca ggg gtg gca gca gac ctc Ser Val Leu Val Gly Glu Glu Leu Tyr Ser Gly Val Ala Ala Asp Leu 180 185 190	814
atg gga cga gac ttt acc atc ttt cgc agc cta ggg caa cgt cca agt Met Gly Arg Asp Phe Thr Ile Phe Arg Ser Leu Gly Gln Arg Pro Ser 195 200 205	862
ctc cga aca gag cca cac gac tcc cgc tgg ctc aat gag ccc aag ttt Leu Arg Thr Glu Pro His Asp Ser Arg Trp Leu Asn Glu Pro Lys Phe 210 215 220 225	910
gtc aag gta ttt tgg atc ccg gag agc gag aac cca gac gac gac aaa Val Lys Val Phe Trp Ile Pro Glu Ser Glu Asn Pro Asp Asp Asp Lys 230 235 240	958
atc tac ttc ttc ttt cgt gag acg gcg gta gag gcg gcg ccg gca ctg Ile Tyr Phe Phe Phe Arg Glu Thr Ala Val Glu Ala Ala Pro Ala Leu 245 250 255	1006
gga cgc ctg tcc gtg tcc cgc gtt ggc cag atc tgc cgg aac gac gtg Gly Arg Leu Ser Val Ser Arg Val Gly Gln Ile Cys Arg Asn Asp Val 260 265 270	1054
ggc ggc cag cgc agc ctg gtc aac aag tgg acg acg ttc ctg aag gcg Gly Gly Gln Arg Ser Leu Val Asn Lys Trp Thr Phe Leu Lys Ala 275 280 285	1102
cgg ctg gtg tgc tcg gtg ccc ggc gtc gag ggc gac acc cac ttc gat Arg Leu Val Cys Ser Val Pro Gly Val Glu Gly Asp Thr His Phe Asp 290 295 300 305	1150
cag ctc cag gat gtg ttt ctg ttg tcc tcg cgg gac cac cgg acc ccg Gln Leu Gln Asp Val Phe Leu Leu Ser Ser Arg Asp His Arg Thr Pro 310 315 320	1198
ctg ctc tat gcc gtc ttc tcc acg tcc agc agc atc ttc cag ggc tct Leu Leu Tyr Ala Val Phe Ser Thr Ser Ser Ser Ile Phe Gln Gly Ser 325 330 335	1246
gcg gtg tgc gtg tac agc atg aac gac gtg cgc cgg gcc ttc ttg gga Ala Val Cys Val Tyr Ser Met Asn Asp Val Arg Arg Ala Phe Leu Gly 340 345 350	1294
ccc ttt gca cac aag gag ggg ccc atg cac cag tgg gtg tca tac cag Pro Phe Ala His Lys Glu Gly Pro Met His Gln Trp Val Ser Tyr Gln 355 360 365	1342
ggt cgc gtc ccc tac ccg cgg cca ggc atg tgc ccc agc aag acc ttt Gly Arg Val Pro Tyr Pro Arg Pro Gly Met Cys Pro Ser Lys Thr Phe 370 375 380 385	1390
ggc acc ttc agt tcc acc aag gac ttc cca gac gat gtc atc cag ttt Gly Thr Phe Ser Ser Thr Lys Asp Phe Pro Asp Asp Val Ile Gln Phe 390 395 400	1438
gcg cgg aac cac ccc ctc atg tac aac tct gtc ctg ccc act ggg ggg Ala Arg Asn His Pro Leu Met Tyr Asn Ser Val Leu Pro Thr Gly Gly 405 410 415	1486
cgc cct ctt ttc cta caa gtt gga gcc aat tac acc ttc act caa att Arg Pro Leu Phe Leu Gln Val Gly Ala Asn Tyr Thr Phe Thr Gln Ile 420 425 430	1534

gcc	gcg	gac	cgg	gtt	gca	gcc	gct	gac	gga	cac	tat	gac	gtc	ctc	ttc	1582
Ala	Ala	Asp	Arg	Val	Ala	Ala	Ala	Asp	Gly	His	Tyr	Asp	Val	Leu	Phe	
435					440					445						
att	ggc	aca	gac	gtt	ggc	acg	gtg	ctg	aag	gtg	atc	tcg	gtc	ccc	aag	1630
Ile	Gly	Thr	Asp	Val	Gly	Thr	Val	Leu	Lys	Val	Ile	Ser	Val	Pro	Lys	
450					455				460						465	
ggc	agt	agg	ccc	agc	gca	gag	ggg	ctg	ctc	ctg	gag	gag	ctg	cac	gtg	1678
Gly	Ser	Arg	Pro	Ser	Ala	Glu	Gly	Leu	Leu	Leu	Glu	Glu	Leu	His	Val	
				470					475					480		
ttt	gag	gac	tcg	gcc	gct	gtc	acc	agc	atg	caa	att	tct	tcc	aag	agg	1726
Phe	Glu	Asp	Ser	Ala	Ala	Val	Thr	Ser	Met	Gln	Ile	Ser	Ser	Lys	Arg	
			485					490					495			
cac	cag	ctg	tac	gta	gcc	tcg	cgg	agc	gcg	gtg	gcc	cag	atc	gcg	ttg	1774
His	Gln	Leu	Tyr	Val	Ala	Ser	Arg	Ser	Ala	Val	Ala	Gln	Ile	Ala	Leu	
			500				505					510				
cac	cgc	tgc	gct	gcc	cac	ggc	cgc	gtc	tgc	acc	gaa	tgc	tgt	ctg	gcg	1822
His	Arg	Cys	Ala	Ala	His	Gly	Arg	Val	Cys	Thr	Glu	Cys	Cys	Leu	Ala	
	515					520					525					
cgt	gac	ccc	tac	tgc	gcc	tgg	gac	ggg	gtc	gcg	tgc	acg	cgc	ttc	cag	1870
Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	Gly	Val	Ala	Cys	Thr	Arg	Phe	Gln	
530					535				540						545	
ccc	agt	gcc	aag	agg	cgg	ttc	cgg	cgg	caa	gac	gta	agg	aat	ggc	gac	1918
Pro	Ser	Ala	Lys	Arg	Arg	Phe	Arg	Arg	Gln	Asp	Val	Arg	Asn	Gly	Asp	
				550					555					560		
ccc	agc	acg	ttg	tgc	tcc	gga	gac	tcg	tct	cgt	ccc	gcg	ctg	ctg	gaa	1966
Pro	Ser	Thr	Leu	Cys	Ser	Gly	Asp	Ser	Ser	Arg	Pro	Ala	Leu	Leu	Glu	
			565				570					575				
cac	aag	gtg	ttc	ggc	gtg	gag	ggc	agc	agc	gcc	ttt	ctg	gag	tgt	gag	2014
His	Lys	Val	Phe	Gly	Val	Glu	Gly	Ser	Ser	Ala	Phe	Leu	Glu	Cys	Glu	
		580					585					590				
ccc	cgc	tcg	ctg	cag	gcg	cgc	gtg	gag	tgg	act	ttc	cag	cgc	gca	ggg	2062
Pro	Arg	Ser	Leu	Gln	Ala	Arg	Val	Glu	Trp	Thr	Phe	Gln	Arg	Ala	Gly	
	595					600					605					
gtg	aca	gcc	cac	acc	cag	gtg	ctg	gca	gag	gag	cgc	acc	gag	cgc	acc	2110
Val	Thr	Ala	His	Thr	Gln	Val	Leu	Ala	Glu	Glu	Arg	Thr	Glu	Arg	Thr	
610					615				620						625	
gcc	cgg	gga	cta	ctg	ctg	cgc	agg	ctg	cgg	cgc	cgg	gac	tcg	ggc	gtg	2158
Ala	Arg	Gly	Leu	Leu	Leu	Arg	Arg	Leu	Arg	Arg	Arg	Asp	Ser	Gly	Val	
				630					635					640		
tac	ttg	tgc	gcc	gcc	gtc	gag	cag	ggc	ttt	acg	caa	ccg	ctg	cgt	cgc	2206
Tyr	Leu	Cys	Ala	Ala	Val	Glu	Gln	Gly	Phe	Thr	Gln	Pro	Leu	Arg	Arg	
			645					650					655			
ctg	tcg	ctg	cac	gtg	ttg	agt	gct	acg	cag	gcc	gaa	cga	ctg	gcg	cgg	2254
Leu	Ser	Leu	His	Val	Leu	Ser	Ala	Thr	Gln	Ala	Glu	Arg	Leu	Ala	Arg	
			660				665				670					
gcc	gag	gag	gct	gcg	ccc	gcc	gcg	ccg	ccg	ggc	ccc	aaa	ctc	tgg	tac	2302
Ala	Glu	Glu	Ala	Ala	Pro	Ala	Ala	Pro	Pro	Gly	Pro	Lys	Leu	Trp	Tyr	
	675					680					685					

cgg gac ttt ctg cag dtg gtg gag ccg ggc gga ggt ggc agc gcg aac 2350  
 Arg Asp Phe Leu Gln Leu Val Glu Pro Gly Gly Gly Gly Ser Ala Asn  
 690 695 700 705

tcc ctg cgc atg tgc cgc ccg cag cct gcg ctg cag tca ctg ccc ctg 2398  
 Ser Leu Arg Met Cys Arg Pro Gln Pro Ala Leu Gln Ser Leu Pro Leu  
 710 715 720

gag tcg cgg aga aag ggc cgt aac cgg agg acc cac gcc cct gag cct 2446  
 Glu Ser Arg Arg Lys Gly Arg Asn Arg Arg Thr His Ala Pro Glu Pro  
 725 730 735

cgc gct gag cgg ggg ccg cgc agc gca acg cac tgg tga ccagactgtc 2495  
 Arg Ala Glu Arg Gly Pro Arg Ser Ala Thr His Trp  
 740 745

cccacgccgg gaaccaagca ggagacgaca ggcgagagag gagccagaca gaccctgaaa 2555

agaaggacgg gttggggccg ggcacattgg gggtcaccgg ccgatggaga caccaaccga 2615

caggccctgg ctgagggcag ctgcgcgggc ttatttatta acaggataac ccttgaatgt 2675

agcagccccg ggagggcggc acaggtcggg cgcaggattc agccggaggg aagggacggg 2735

gaagccgagc tccagagcaa cgaccagggc cgaggaggtg cctggagtgc ccaccctggg 2795

agacagaccc cacctccttg ggtagtgagc agtgagcaga aagctgtgaa caggctgggc 2855

tgctggaggt ggggcgaggc aggccgactg tactaaagta acgcaataaa cgcattatca 2915

gcca 2919

<210> 12

<211> 749

<212> PRT

<213> Homo. sapiens

<400> 12

Met Gly Arg Ala Gly Ala Ala Ala Val Ile Pro Gly Leu Ala Leu Leu  
 1 5 10 15

Trp Ala Val Gly Leu Gly Ser Ala Ala Pro Ser Pro Pro Arg Leu Arg  
 20 25 30

Leu Ser Phe Gln Glu Leu Gln Ala Trp His Gly Leu Gln Thr Phe Ser  
 35 40 45

Leu Glu Arg Thr Cys Cys Tyr Gln Ala Leu Leu Val Asp Glu Glu Arg  
 50 55 60

Gly Arg Leu Phe Val Gly Ala Glu Asn His Val Ala Ser Leu Asn Leu  
 65 70 75 80

Asp Asn Ile Ser Lys Arg Ala Lys Lys Leu Ala Trp Pro Ala Pro Val  
 85 90 95

Glu Trp Arg Glu Glu Cys Asn Trp Ala Gly Lys Asp Ile Gly Thr Glu  
 100 105 110

Cys Met Asn Phe Val Lys Leu Leu His Ala Tyr Asn Arg Thr His Leu  
 115 120 125

Leu Ala Cys Gly Thr Gly Ala Phe His Pro Thr Cys Ala Phe Val Glu  
 130 135 140

Val Gly His Arg Ala Glu Glu Pro Val Leu Arg Leu Asp Pro Gly Arg  
 145 150 155 160

Ile Glu Asp Gly Lys Gly Lys Ser Pro Tyr Asp Pro Arg His Arg Ala  
 165 170 175

Ala Ser Val Leu Val Gly Glu Glu Leu Tyr Ser Gly Val Ala Ala Asp  
 180 185 190

Leu Met Gly Arg Asp Phe Thr Ile Phe Arg Ser Leu Gly Gln Arg Pro  
 195 200 205

Ser Leu Arg Thr Glu Pro His Asp Ser Arg Trp Leu Asn Glu Pro Lys  
 210 215 220

Phe Val Lys Val Phe Trp Ile Pro Glu Ser Glu Asn Pro Asp Asp Asp  
 225 230 235 240

Lys Ile Tyr Phe Phe Phe Arg Glu Thr Ala Val Glu Ala Ala Pro Ala  
 245 250 255

Leu Gly Arg Leu Ser Val Ser Arg Val Gly Gln Ile Cys Arg Asn Asp  
 260 265 270

Val Gly Gly Gln Arg Ser Leu Val Asn Lys Trp Thr Thr Phe Leu Lys  
 275 280 285

Ala Arg Leu Val Cys Ser Val Pro Gly Val Glu Gly Asp Thr His Phe  
 290 295 300

Asp Gln Leu Gln Asp Val Phe Leu Leu Ser Ser Arg Asp His Arg Thr  
 305 310 315 320

Pro Leu Leu Tyr Ala Val Phe Ser Thr Ser Ser Ser Ile Phe Gln Gly  
 325 330 335

Ser Ala Val Cys Val Tyr Ser Met Asn Asp Val Arg Arg Ala Phe Leu  
 340 345 350

Gly Pro Phe Ala His Lys Glu Gly Pro Met His Gln Trp Val Ser Tyr  
 355 360 365

Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Met Cys Pro Ser Lys Thr  
 370 375 380

Phe Gly Thr Phe Ser Ser Thr Lys Asp Phe Pro Asp Asp Val Ile Gln  
 385 390 395 400

Phe Ala Arg Asn His Pro Leu Met Tyr Asn Ser Val Leu Pro Thr Gly  
 405 410 415

Gly Arg Pro Leu Phe Leu Gln Val Gly Ala Asn Tyr Thr Phe Thr Gln  
 420 425 430

Ile Ala Ala Asp Arg Val Ala Ala Ala Asp Gly His Tyr Asp Val Leu  
 435 440 445

Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys Val Ile Ser Val Pro  
 450 455 460

Lys Gly Ser Arg Pro Ser Ala Glu Gly Leu Leu Leu Glu Glu Leu His  
 465 470 475 480

Val Phe Glu Asp Ser Ala Ala Val Thr Ser Met Gln Ile Ser Ser Lys  
 485 490 495

Arg His Gln Leu Tyr Val Ala Ser Arg Ser Ala Val Ala Gln Ile Ala  
 500 505 510

Leu His Arg Cys Ala Ala His Gly Arg Val Cys Thr Glu Cys Cys Leu  
 515 520 525

Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Val Ala Cys Thr Arg Phe  
 530 535 540

Gln Pro Ser Ala Lys Arg Arg Phe Arg Arg Gln Asp Val Arg Asn Gly  
 545 550 555 560

Asp Pro Ser Thr Leu Cys Ser Gly Asp Ser Ser Arg Pro Ala Leu Leu  
 565 570 575

Glu His Lys Val Phe Gly Val Glu Gly Ser Ser Ala Phe Leu Glu Cys  
 580 585 590

Glu Pro Arg Ser Leu Gln Ala Arg Val Glu Trp Thr Phe Gln Arg Ala  
 595 600 605

Gly Val Thr Ala His Thr Gln Val Leu Ala Glu Glu Arg Thr Glu Arg  
610 615 620

Thr Ala Arg Gly Leu Leu Leu Arg Arg Leu Arg Arg Arg Asp Ser Gly  
625 630 635 640

Val Tyr Leu Cys Ala Ala Val Glu Gln Gly Phe Thr Gln Pro Leu Arg  
645 650 655

Arg Leu Ser Leu His Val Leu Ser Ala Thr Gln Ala Glu Arg Leu Ala  
660 665 670

Arg Ala Glu Glu Ala Ala Pro Ala Ala Pro Pro Gly Pro Lys Leu Trp  
675 680 685

Tyr Arg Asp Phe Leu Gln Leu Val Glu Pro Gly Gly Gly Gly Ser Ala  
690 695 700

Asn Ser Leu Arg Met Cys Arg Pro Gln Pro Ala Leu Gln Ser Leu Pro  
705 710 715 720

Leu Glu Ser Arg Arg Lys Gly Arg Asn Arg Arg Thr His Ala Pro Glu  
725 730 735

Pro Arg Ala Glu Arg Gly Pro Arg Ser Ala Thr His Trp  
740 745

<210> 13  
<211> 5177  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (563)..(2818)

<400> 13  
ggactgcgaa aggagcaggg ttgcggagct agggctccag cctgcggccg cgcattcttg 60  
cgtctggcca gccgcgagct ctaagggctg gccccgcccc gtccgcccc gcggtccct 120  
gccaggctct cgcgggcgcg ctcggggtgg ggcctcgcg ctggcggaga tgcggccggg 180  
gctgcgcggt ggtgatgcga gcctgctggg cggcgcgccg gggcagccgg agccgcgcgc 240  
cgcgggcgctg taatcgga ccaagagcgc tcgcccccg cctccggcca ctttccattc 300  
actccgaggt gcttgattga gcgacgcgga gaagagctcc ggggtgccgcg gcaactgcgc 360  
gctgagattc ctttaciaaag aaactcagag gaccgggaag aaagaatttc acctttgcga 420  
cgtgctagaa aataaggtcg tctgggaaaa ggactggaga cacaagcgca tccaaccccg 480

gtagcaaact gatgactttt ccgtgctgat ttctttcaac ctcggtatatt tcccttgat	540
attaacttgc atatctgaag aa atg gca ttc cgg aca att tgc gtg ttg gtt Met Ala Phe Arg Thr Ile Cys Val Leu Val 1 5 10	592
gga gta ttt att tgt tct atc tgt gtg aaa gga tct tcc cag ccc caa Gly Val Phe Ile Cys Ser Ile Cys Val Lys Gly Ser Ser Gln Pro Gln 15 20 25	640
gca aga gtt tat tta aca ttt gat gaa ctt cga gaa acc aag acc tct Ala Arg Val Tyr Leu Thr Phe Asp Glu Leu Arg Glu Thr Lys Thr Ser 30 35 40	688
gaa tac ttc agc ctt tcc cac cat cct tta gac tac agg att tta tta Glu Tyr Phe Ser Leu Ser His His Pro Leu Asp Tyr Arg Ile Leu Leu 45 50 55	736
atg gat gaa gat cag gac cgg ata tat gtg gga agc aaa gat cac att Met Asp Glu Asp Gln Asp Arg Ile Tyr Val Gly Ser Lys Asp His Ile 60 65 70	784
ctt tcc ctg aat att aac aat ata agt caa gaa gct ttg agt gtt ttc Leu Ser Leu Asn Ile Asn Asn Ile Ser Gln Glu Ala Leu Ser Val Phe 75 80 85 90	832
tgg cca gca tct aca atc aaa gtt gaa gaa tgc aaa atg gct ggc aaa Trp Pro Ala Ser Thr Ile Lys Val Glu Glu Cys Lys Met Ala Gly Lys 95 100 105	880
gat ccc aca cac ggc tgt ggg aac ttt gtc cgt gta att cag act ttc Asp Pro Thr His Gly Cys Gly Asn Phe Val Arg Val Ile Gln Thr Phe 110 115 120	928
aat cgc aca cat ttg tat gtc tgt ggg agt ggc gct ttc agt cct gtc Asn Arg Thr His Leu Tyr Val Cys Gly Ser Gly Ala Phe Ser Pro Val 125 130 135	976
tgt act tac ttg aac aga ggg agg aga tca gag gac caa gtt ttc atg Cys Thr Tyr Leu Asn Arg Gly Arg Arg Ser Glu Asp Gln Val Phe Met 140 145 150	1024
att gac tcc aag tgt gaa tct gga aaa gga cgc tgc tct ttc aac ccc Ile Asp Ser Lys Cys Glu Ser Gly Lys Gly Arg Cys Ser Phe Asn Pro 155 160 165 170	1072
aac gtg aac acg gtg tct gtt atg atc aat gag gag ctt ttc tct gga Asn Val Asn Thr Val Ser Val Met Ile Asn Glu Glu Leu Phe Ser Gly 175 180 185	1120
atg tat ata gat ttc atg ggg aca gat gct gct att ttt cga agt tta Met Tyr Ile Asp Phe Met Gly Thr Asp Ala Ala Ile Phe Arg Ser Leu 190 195 200	1168
acc aag agg aat gcg gtc aga act gat caa cat aat tcc aaa tgg cta Thr Lys Arg Asn Ala Val Arg Thr Asp Gln His Asn Ser Lys Trp Leu 205 210 215	1216
agt gaa cct atg ttt gta gat gca cat gtc atc cca gat ggt act gat Ser Glu Pro Met Phe Val Asp Ala His Val Ile Pro Asp Gly Thr Asp 220 225 230	1264

cca aat gat gct aag gtg tac ttc ttc ttc aaa gaa aaa ctg act gac	1312
Pro Asn Asp Ala Lys Val Tyr Phe Phe Phe Lys Glu Lys Leu Thr Asp	
235 240 245 250	
aat aac agg agc acg aaa cag att cat tcc atg att gct cga ata tgt	1360
Asn Asn Arg Ser Thr Lys Gln Ile His Ser Met Ile Ala Arg Ile Cys	
255 260 265	
cct aat gac act ggt gga ctg cgt agc ctt gtc aac aag tgg acc act	1408
Pro Asn Asp Thr Gly Gly Leu Arg Ser Leu Val Asn Lys Trp Thr Thr	
270 275 280	
ttc tta aag gcg agg ctg gtg tgc tcg gta aca gat gaa gac ggc cca	1456
Phe Leu Lys Ala Arg Leu Val Cys Ser Val Thr Asp Glu Asp Gly Pro	
285 290 295	
gaa aca cac ttt gat gaa tta gag gat gtg ttt ctg ctg gaa act gat	1504
Glu Thr His Phe Asp Glu Leu Glu Asp Val Phe Leu Leu Glu Thr Asp	
300 305 310	
aac ccg agg aca aca cta gtg tat ggc att ttt aca aca tca agc tca	1552
Asn Pro Arg Thr Thr Leu Val Tyr Gly Ile Phe Thr Thr Ser Ser Ser	
315 320 325 330	
gtt ttc aaa gga tca gcc gtg tgt gtg tat cat tta tct gat ata cag	1600
Val Phe Lys Gly Ser Ala Val Cys Val Tyr His Leu Ser Asp Ile Gln	
335 340 345	
act gtg ttt aat ggg cct ttt gcc cac aaa gaa ggg ccc aat cat cag	1648
Thr Val Phe Asn Gly Pro Phe Ala His Lys Glu Gly Pro Asn His Gln	
350 355 360	
ctg att tcc tat cag ggc aga att cca tat cct cgc cct gga act tgt	1696
Leu Ile Ser Tyr Gln Gly Arg Ile Pro Tyr Pro Arg Pro Gly Thr Cys	
365 370 375	
cca gga gga gca ttt aca ccc aat atg cga acc acc aag gag ttc cca	1744
Pro Gly Gly Ala Phe Thr Pro Asn Met Arg Thr Thr Lys Glu Phe Pro	
380 385 390	
gat gat gtt gtc act ttt att cgg aac cat cct ctc atg tac aat tcc	1792
Asp Asp Val Val Thr Phe Ile Arg Asn His Pro Leu Met Tyr Asn Ser	
395 400 405 410	
atc tac cca atc cac aaa agg cct ttg att gtt cgt att ggc act gac	1840
Ile Tyr Pro Ile His Lys Arg Pro Leu Ile Val Arg Ile Gly Thr Asp	
415 420 425	
tac aag tac aca aag ata gct gtg gat cga gtg aac gct gct gat ggg	1888
Tyr Lys Tyr Thr Lys Ile Ala Val Asp Arg Val Asn Ala Ala Asp Gly	
430 435 440	
aga tac cat gtc ctg ttt ctc gga aca gat cgg ggt act gtg caa aaa	1936
Arg Tyr His Val Leu Phe Leu Gly Thr Asp Arg Gly Thr Val Gln Lys	
445 450 455	
gtg gtt gtt ctt cct act aac aac tct gtc agt ggc gag ctc att ctg	1984
Val Val Val Leu Pro Thr Asn Asn Ser Val Ser Gly Glu Leu Ile Leu	
460 465 470	
gag gag ctg gaa gtc ttt aag aat cat gct cct ata aca aca atg aaa	2032
Glu Glu Leu Glu Val Phe Lys Asn His Ala Pro Ile Thr Thr Met Lys	
475 480 485 490	



att tca tct aaa aag caa cag ttg tat gtg agt tcc aat gaa ggg gtt Ile Ser Ser Lys Lys Gln Gln Leu Tyr Val Ser Ser Asn Glu Gly Val 495 500 505	2080
tcc caa gta tct ctg cac cgc tgc cac atc tat ggt aca gcc tgt gct Ser Gln Val Ser Leu His Arg Cys His Ile Tyr Gly Thr Ala Cys Ala 510 515 520	2128
gac tgc tgc ctg gcg cgg gac cct tat tgc gcc tgg gat ggc cat tcc Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly His Ser 525 530 535	2176
tgt tcc aga ttc tac cca act ggg aaa cgg agg agc cga aga caa gat Cys Ser Arg Phe Tyr Pro Gly Lys Arg Arg Ser Arg Arg Gln Asp 540 545 550	2224
gtg aga cat gga aac cca ctg act caa tgc aga gga ttt aat cta aaa Val Arg His Gly Asn Pro Leu Thr Gln Cys Arg Gly Phe Asn Leu Lys 555 560 565 570	2272
gca tac aga aat gca gct gaa att gtg cag tat gga gta aaa aat aac Ala Tyr Arg Asn Ala Ala Glu Ile Val Gln Tyr Gly Val Lys Asn Asn 575 580 585	2320
acc act ttt ctg gag tgt gcc ccc aag tct ccg cag gca tct atc aag Thr Thr Phe Leu Glu Cys Ala Pro Lys Ser Pro Gln Ala Ser Ile Lys 590 595 600	2368
tgg ctg tta cag aaa gac aaa gac agg agg aaa gag gtt aag ctg aat Trp Leu Leu Gln Lys Asp Lys Asp Arg Arg Lys Glu Val Lys Leu Asn 605 610 615	2416
gaa cga ata ata gcc act tca cag gga ctc ctg atc cgc tct gtt cag Glu Arg Ile Ile Ala Thr Ser Gln Gly Leu Leu Ile Arg Ser Val Gln 620 625 630	2464
ggg tct gac caa gga ctt tat cac tgc att gct aca gaa aat agt ttc Gly Ser Asp Gln Gly Leu Tyr His Cys Ile Ala Thr Glu Asn Ser Phe 635 640 645 650	2512
aag cag acc ata gcc aag atc aac ttc aaa gtt tta gat tca gaa atg Lys Gln Thr Ile Ala Lys Ile Asn Phe Lys Val Leu Asp Ser Glu Met 655 660 665	2560
gtg gct gtt gtg acg gac aaa tgg tcc ccg tgg acc tgg gcc agc tct Val Ala Val Val Thr Asp Lys Trp Ser Pro Trp Thr Trp Ala Ser Ser 670 675 680	2608
gtg agg gct tta ccc ttc cac ccg aag gac atc atg ggg gca ttc agc Val Arg Ala Leu Pro Phe His Pro Lys Asp Ile Met Gly Ala Phe Ser 685 690 695	2656
cac tca gaa atg cag atg att aac caa tac tgc aaa gac act cgg cag His Ser Glu Met Gln Met Ile Asn Gln Tyr Cys Lys Asp Thr Arg Gln 700 705 710	2704
caa cat cag cag gga gat gaa tca cag aaa atg aga ggg gac tat ggc Gln His Gln Gln Gly Asp Glu Ser Gln Lys Met Arg Gly Asp Tyr Gly 715 720 725 730	2752
aag tta aag gcc ctc atc aat agt cgg aaa agt aga aac agg agg aat Lys Leu Lys Ala Leu Ile Asn Ser Arg Lys Ser Arg Asn Arg Arg Asn 735 740 745	2800

cag ttg cca gag tca taa ttttttctta tgtgggtctt atgcttccat 2848  
 Gln Leu Pro Glu Ser  
 750

taacaaatgc tctgtcttca atgatcaa at tttgagcaaa gaaacttgtg ctttaccaag 2908  
 ggggaattact gaaaaagggtg attactcctg aagtgagttt tacacgaact gaaatgagca 2968  
 tgcatttttct tgtatgatag tgactagcac tagacatgtc atgggtcctca tgggtgcatat 3028  
 aaatatattt aacttaaccc agattttatt tataatcttta ttcacctttt cttcaaaatc 3088  
 gatatgggtg ctgcaaaact agaattgttg catccctcaa ttgaatgagg gccatatccc 3148  
 tgtggtattc ctttcctgct ttgggggcttt agaattctaa ttgtcagtga ttttgtatat 3208  
 gaaaacaagt tccaaatcca cagctttttac gtagtaaaag tcataaatgc atatgacaga 3268  
 atggctatca aaagaaatag aaaaggaaga cggcatttaa agttgtataa aaacacgagt 3328  
 tattcataaa gagaaaatga tgagttttta tggttccaat gaaatatctt cccctttttt 3388  
 taagattgta aaaataatca gttactggta tctgtcactg acctttgttt ccttattcag 3448  
 gaagataaaa atcagtaacc taccocatga agatatttgg tgggagttat atcagtgaag 3508  
 cagtttggtt tatattctta tgttatcacc ttccaaacaa aagcacttac tttttttgga 3568  
 agttatttaa tttatttttag actcaaagaa tataatcttg cactactcag ttattactgt 3628  
 ttgttctctt attccctagt ctgtgtggca aattaaacaa tataagaagg aaaaatttga 3688  
 agtattagac ttctaaataa ggggtgaaat catcagaaag aaaaatcaaa gtagaaacta 3748  
 ctaatttttt aagaggaatt tataacaaat atggctagtt ttcaacttca gtactcaaat 3808  
 tcaatgattc ttctttttat taaaaccagt ctcatatc atactgattt ttaagtcaac 3868  
 actatatatt ttatgatctt ttcagtgtga tggcaagggtg cttgttatgt ctagaaagta 3928  
 agaaaacaat atgaggagac attctgtctt tcaaaaggta atggtacata cgttccactgg 3988  
 tctctaagtg taaaagtagt aaattttgtg atgaataaaa taattatctc ctaattgtat 4048  
 gttagaataa ttttattaga ataatttcat actgaaatta ttttctccaa ataaaaatta 4108  
 gatggaaaaa tgtgaaaaaa attattcatg ctctcatata ttttttaaaa acactacttt 4168  
 tgctttttta tttacctttt aagacatttt catgcttcca ggtaaaaaca gatattgtac 4228  
 catgtacctt atccaaatat catataaaca ttttatttat agttaataat ctatgatgaa 4288  
 ggtaattaaa gtagattatg gcctttttta gtattgcagt ctaaaacttc aaaaactaaa 4348  
 atcattgtca aaattaatat gattattaat cagaatatca gatatgattc actattttaa 4408  
 ctatgataaa ttatgataat atatgaggag gcctcgctat agcaaaaata gttaaaatgc 4468  
 tgacataaca ccaaacttca ttttttaaaa aatctgttgt tccaaatgtg tataatttta 4528  
 aagtaatttc taaagcagtt tattataatg gtttgcctgc ttaaaaggta taattaaact 4588  
 tcttttctct tctacattga cacacagaaa tgtgtcaatg taaagccaaa accatcttct 4648

```

gtgtttatgg ccaatctatt ctcaaagtta aaagtaaaat tgtttcagag tcacagttcc 4708
ctttattttca cataagccca aactgataga cagtaacggg gtttagtttt atactatatt 4768
tgtgctattt aattctttct attttcacaa ttattaaatt gtgtacactt tcattacttt 4828
taaaaatgta gaaattcttc atgaacataa ctctgctgaa tgtaaaagaa aatttttttt 4888
caaaaatgct gttaatgtat actactgggt gttgattggg tttattttat gtagcttgac 4948
aattcagtga cttaatatct attccatttg tattgtacat aaaattttct agaaatacac 5008
ttttttccaa agtgtaagtt tgtgaataga ttttagcatg atgaaactgt cataatgggtg 5068
aatgttcaat ctgtgtaaga aaacaaacta aatgtagttg tcacactaaa atttaattgg 5128
atattgatga aatcattggc ctggcaaaat aaaacatggt gaattcccc 5177

```

&lt;210&gt; 14

&lt;211&gt; 751

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

```

Met Ala Phe Arg Thr Ile Cys Val Leu Val Gly Val Phe Ile Cys Ser
1           5           10           15

```

```

Ile Cys Val Lys Gly Ser Ser Gln Pro Gln Ala Arg Val Tyr Leu Thr
          20           25           30

```

```

Phe Asp Glu Leu Arg Glu Thr Lys Thr Ser Glu Tyr Phe Ser Leu Ser
          35           40           45

```

```

His His Pro Leu Asp Tyr Arg Ile Leu Leu Met Asp Glu Asp Gln Asp
          50           55           60

```

```

Arg Ile Tyr Val Gly Ser Lys Asp His Ile Leu Ser Leu Asn Ile Asn
65           70           75           80

```

```

Asn Ile Ser Gln Glu Ala Leu Ser Val Phe Trp Pro Ala Ser Thr Ile
          85           90           95

```

```

Lys Val Glu Glu Cys Lys Met Ala Gly Lys Asp Pro Thr His Gly Cys
          100          105          110

```

```

Gly Asn Phe Val Arg Val Ile Gln Thr Phe Asn Arg Thr His Leu Tyr
          115          120          125

```

```

Val Cys Gly Ser Gly Ala Phe Ser Pro Val Cys Thr Tyr Leu Asn Arg
          130          135          140

```

Gly Arg Arg Ser Glu Asp Gln Val Phe Met Ile Asp Ser Lys Cys Glu  
145 150 155 160

Ser Gly Lys Gly Arg Cys Ser Phe Asn Pro Asn Val Asn Thr Val Ser  
165 170 175

Val Met Ile Asn Glu Glu Leu Phe Ser Gly Met Tyr Ile Asp Phe Met  
180 185 190

Gly Thr Asp Ala Ala Ile Phe Arg Ser Leu Thr Lys Arg Asn Ala Val  
195 200 205

Arg Thr Asp Gln His Asn Ser Lys Trp Leu Ser Glu Pro Met Phe Val  
210 215 220

Asp Ala His Val Ile Pro Asp Gly Thr Asp Pro Asn Asp Ala Lys Val  
225 230 235 240

Tyr Phe Phe Phe Lys Glu Lys Leu Thr Asp Asn Asn Arg Ser Thr Lys  
245 250 255

Gln Ile His Ser Met Ile Ala Arg Ile Cys Pro Asn Asp Thr Gly Gly  
260 265 270

Leu Arg Ser Leu Val Asn Lys Trp Thr Thr Phe Leu Lys Ala Arg Leu  
275 280 285

Val Cys Ser Val Thr Asp Glu Asp Gly Pro Glu Thr His Phe Asp Glu  
290 295 300

Leu Glu Asp Val Phe Leu Leu Glu Thr Asp Asn Pro Arg Thr Thr Leu  
305 310 315 320

Val Tyr Gly Ile Phe Thr Thr Ser Ser Ser Val Phe Lys Gly Ser Ala  
325 330 335

Val Cys Val Tyr His Leu Ser Asp Ile Gln Thr Val Phe Asn Gly Pro  
340 345 350

Phe Ala His Lys Glu Gly Pro Asn His Gln Leu Ile Ser Tyr Gln Gly  
355 360 365

Arg Ile Pro Tyr Pro Arg Pro Gly Thr Cys Pro Gly Gly Ala Phe Thr  
370 375 380

Pro Asn Met Arg Thr Thr Lys Glu Phe Pro Asp Asp Val Val Thr Phe  
385 390 395 400

Ile Arg Asn His Pro Leu Met Tyr Asn Ser Ile Tyr Pro Ile His Lys  
 405 410 415

Arg Pro Leu Ile Val Arg Ile Gly Thr Asp Tyr Lys Tyr Thr Lys Ile  
 420 425 430

Ala Val Asp Arg Val Asn Ala Ala Asp Gly Arg Tyr His Val Leu Phe  
 435 440 445

Leu Gly Thr Asp Arg Gly Thr Val Gln Lys Val Val Val Leu Pro Thr  
 450 455 460

Asn Asn Ser Val Ser Gly Glu Leu Ile Leu Glu Glu Leu Glu Val Phe  
 465 470 475 480

Lys Asn His Ala Pro Ile Thr Thr Met Lys Ile Ser Ser Lys Lys Gln  
 485 490 495

Gln Leu Tyr Val Ser Ser Asn Glu Gly Val Ser Gln Val Ser Leu His  
 500 505 510

Arg Cys His Ile Tyr Gly Thr Ala Cys Ala Asp Cys Cys Leu Ala Arg  
 515 520 525

Asp Pro Tyr Cys Ala Trp Asp Gly His Ser Cys Ser Arg Phe Tyr Pro  
 530 535 540

Thr Gly Lys Arg Arg Ser Arg Arg Gln Asp Val Arg His Gly Asn Pro  
 545 550 555 560

Leu Thr Gln Cys Arg Gly Phe Asn Leu Lys Ala Tyr Arg Asn Ala Ala  
 565 570 575

Glu Ile Val Gln Tyr Gly Val Lys Asn Asn Thr Thr Phe Leu Glu Cys  
 580 585 590

Ala Pro Lys Ser Pro Gln Ala Ser Ile Lys Trp Leu Leu Gln Lys Asp  
 595 600 605

Lys Asp Arg Arg Lys Glu Val Lys Leu Asn Glu Arg Ile Ile Ala Thr  
 610 615 620

Ser Gln Gly Leu Leu Ile Arg Ser Val Gln Gly Ser Asp Gln Gly Leu  
 625 630 635 640

Tyr His Cys Ile Ala Thr Glu Asn Ser Phe Lys Gln Thr Ile Ala Lys  
 645 650 655

Ile Asn Phe Lys Val Leu Asp Ser Glu Met Val Ala Val Val Thr Asp  
660 665 670

Lys Trp Ser Pro Trp Thr Trp Ala Ser Ser Val Arg Ala Leu Pro Phe  
675 680 685

His Pro Lys Asp Ile Met Gly Ala Phe Ser His Ser Glu Met Gln Met  
690 695 700

Ile Asn Gln Tyr Cys Lys Asp Thr Arg Gln Gln His Gln Gln Gly Asp  
705 710 715 720

Glu Ser Gln Lys Met Arg Gly Asp Tyr Gly Lys Leu Lys Ala Leu Ile  
725 730 735

Asn Ser Arg Lys Ser Arg Asn Arg Arg Asn Gln Leu Pro Glu Ser  
740 745 750

<210> 15  
<211> 6474  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (467)..(2794)

<400> 15  
gtttggcaag tcagtgcaag aggctgactt ctgagaggct tccaggagcc cgaagagagg 60  
acctccacgg gagaagggag tgcgtgtgct cggttttttt tttttctctc tttttttttt 120  
ttttttctga atgaacagct ttgcccaagt gactgaaaaa tacagcttct tcctgaatct 180  
accggcgtag ttgctgaaga gcgctctaga caggacatgg ctctgaagac tcactctttg 240  
gaatgtcctc ttgctcccgg cttataaaca actgtcccga ggaaagaaaag gttttacata 300  
gccaaataca gcctgacaaa tggcacttcg gaactgtgct ttctgatgac aacgcgttcg 360  
atttctgaca aagcctctcg cacgctgccc ctggagggaa gtcctaagta aaactcagac 420  
cctccttaaa gtgaggagcg agggcttgga cgggtgaacac ggcagc atg gca tcc 475  
Met Ala Ser  
1

gcg ggg cac att atc acc ttg ctc ctg tgg ggt tac tta ctg gag ctt 523  
Ala Gly His Ile Ile Thr Leu Leu Leu Trp Gly Tyr Leu Leu Glu Leu  
5 10 15

tgg aca gga ggt cat aca gct gat act acc cac ccc cgg tta cgc ctg 571  
Trp Thr Gly Gly His Thr Ala Asp Thr Thr His Pro Arg Leu Arg Leu  
20 25 30 35

tca cat aaa gag ctc ttg aat ctg aac aga aca tca ata ttt cat agc 619  
Ser His Lys Glu Leu Leu Asn Leu Asn Arg Thr Ser Ile Phe His Ser  
40 45 50

cct ttt gga ttt ctt gat ctc cat aca atg ctg ctg gat gaa tat caa Pro Phe Gly Phe Leu Asp Leu His Thr Met Leu Leu Asp Glu Tyr Gln 55 60 65	667
gag agg ctc ttc gtg gga ggc agg gac ctt gta tat tcc ctc agc ttg Glu Arg Leu Phe Val Gly Gly Arg Asp Leu Val Tyr Ser Leu Ser Leu 70 75 80	715
gag aga atc agt gac ggc tat aaa gag ata cac tgg ccg agt aca gct Glu Arg Ile Ser Asp Gly Tyr Lys Glu Ile His Trp Pro Ser Thr Ala 85 90 95	763
cta aaa atg gaa gaa tgc ata atg aag gga aaa gat gcg ggt gaa tgt Leu Lys Met Glu Glu Cys Ile Met Lys Gly Lys Asp Ala Gly Glu Cys 100 105 110 115	811
gca aat tat gtt cgg gtt ttg cat cac tat aac agg aca cac ctt ctg Ala Asn Tyr Val Arg Val Leu His His Tyr Asn Arg Thr His Leu Leu 120 125 130	859
acc tgt ggt act gga gct ttt gat cca gtt tgt gcc ttc atc aga gtt Thr Cys Gly Thr Gly Ala Phe Asp Pro Val Cys Ala Phe Ile Arg Val 135 140 145	907
gga tat cat ttg gag gat cct ctg ttt cac ctg gaa tca ccc aga tct Gly Tyr His Leu Glu Asp Pro Leu Phe His Leu Glu Ser Pro Arg Ser 150 155 160	955
gag aga gga agg ggc aga tgt cct ttt gac ccc agc tcc tcc ttc atc Glu Arg Gly Arg Gly Arg Cys Pro Phe Asp Pro Ser Ser Ser Phe Ile 165 170 175	1003
tcc act tta att ggt agt gaa ttg ttt gct gga ctc tac agt gac tac Ser Thr Leu Ile Gly Ser Glu Leu Phe Ala Gly Leu Tyr Ser Asp Tyr 180 185 190 195	1051
tgg agc aga gac gct gcg atc ttc cgc agc atg ggg cga ctg gcc cat Trp Ser Arg Asp Ala Ala Ile Phe Arg Ser Met Gly Arg Leu Ala His 200 205 210	1099
atc cgc act gag cat gac gat gag cgt ctg ttg aaa gaa cca aaa ttt Ile Arg Thr Glu His Asp Asp Glu Arg Leu Leu Lys Glu Pro Lys Phe 215 220 225	1147
gta ggt tca tac atg att cct gac aat gaa gac aga gat gac aac aaa Val Gly Ser Tyr Met Ile Pro Asp Asn Glu Asp Arg Asp Asp Asn Lys 230 235 240	1195
gta tat ttc ttt ttt act gag aag gca ctg gag gca gaa aac aat gct Val Tyr Phe Phe Phe Thr Glu Lys Ala Leu Glu Ala Glu Asn Asn Ala 245 250 255	1243
cac gca att tac acc agg gtc ggg cga ctc tgt gtg aat gat gta gga His Ala Ile Tyr Thr Arg Val Gly Arg Leu Cys Val Asn Asp Val Gly 260 265 270 275	1291
ggg cag aga ata ctg gtg aat aag tgg agc act ttc cta aaa gcg aga Gly Gln Arg Ile Leu Val Asn Lys Trp Ser Thr Phe Leu Lys Ala Arg 280 285 290	1339
ctc gtt tgc tca gta cca gga atg aat gga att gac aca tat ttt gat	1387

Leu	Val	Cys	Ser	Val	Pro	Gly	Met	Asn	Gly	Ile	Asp	Thr	Tyr	Phe	Asp	
			295					300					305			
gaa	tta	gag	gac	gtt	ttt	ttg	cta	cct	acc	aga	gat	cat	aag	aat	cca	1435
Glu	Leu	Glu	Asp	Val	Phe	Leu	Leu	Pro	Thr	Arg	Asp	His	Lys	Asn	Pro	
		310				315					320					
gtg	ata	ttt	gga	ctc	ttt	aac	act	acc	agt	aat	att	ttt	cga	ggg	cat	1483
Val	Ile	Phe	Gly	Leu	Phe	Asn	Thr	Thr	Ser	Asn	Ile	Phe	Arg	Gly	His	
	325					330					335					
gct	ata	tgt	gtc	tat	cac	atg	tct	agc	att	cgg	gca	gcc	ttc	aac	gga	1531
Ala	Ile	Cys	Val	Tyr	His	Met	Ser	Ser	Ile	Arg	Ala	Ala	Phe	Asn	Gly	
340					345					350					355	
cca	tat	gca	cat	aag	gaa	gga	cct	gaa	tac	cac	tgg	tca	gtc	tat	gaa	1579
Pro	Tyr	Ala	His	Lys	Glu	Gly	Pro	Glu	Tyr	His	Trp	Ser	Val	Tyr	Glu	
				360					365					370		
gga	aaa	gtc	cct	tat	cca	agg	cct	ggt	tct	tgt	gcc	agc	aaa	gta	aat	1627
Gly	Lys	Val	Pro	Tyr	Pro	Arg	Pro	Gly	Ser	Cys	Ala	Ser	Lys	Val	Asn	
			375					380					385			
gga	ggg	aga	tac	gga	acc	acc	aag	gac	tat	cct	gat	gat	gcc	atc	cga	1675
Gly	Gly	Arg	Tyr	Gly	Thr	Thr	Lys	Asp	Tyr	Pro	Asp	Ala	Ala	Ile	Arg	
		390					395				400					
ttt	gca	aga	agt	cat	cca	cta	atg	tac	cag	gcc	ata	aaa	cct	gcc	cat	1723
Phe	Ala	Arg	Ser	His	Pro	Leu	Met	Tyr	Gln	Ala	Ile	Lys	Pro	Ala	His	
	405					410					415					
aaa	aaa	cca	ata	ttg	gta	aaa	aca	gat	gga	aaa	tat	aac	ctg	aaa	caa	1771
Lys	Lys	Pro	Ile	Leu	Val	Lys	Thr	Asp	Gly	Lys	Tyr	Asn	Leu	Lys	Gln	
420				425					430						435	
ata	gca	gta	gat	cga	gtg	gaa	gct	gag	gat	ggc	caa	tat	gac	gtc	ttg	1819
Ile	Ala	Val	Asp	Arg	Val	Glu	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	Val	Leu	
				440				445						450		
ttt	att	ggg	aca	gat	aat	gga	att	gtg	ctg	aaa	gta	atc	aca	att	tac	1867
Phe	Ile	Gly	Thr	Asp	Asn	Gly	Ile	Val	Leu	Lys	Val	Ile	Thr	Ile	Tyr	
			455					460					465			
aac	caa	gaa	atg	gaa	tca	atg	gaa	gaa	gta	att	cta	gaa	gaa	ctt	cag	1915
Asn	Gln	Glu	Met	Glu	Ser	Met	Glu	Glu	Val	Ile	Leu	Glu	Glu	Leu	Gln	
		470				475					480					
ata	ttc	aag	gat	cca	gtt	cct	att	att	tct	atg	gag	att	tct	tca	aaa	1963
Ile	Phe	Lys	Asp	Pro	Val	Pro	Ile	Ile	Ser	Met	Glu	Ile	Ser	Ser	Lys	
	485					490					495					
cgg	caa	cag	ctg	tat	att	gga	tct	gct	tct	gct	gtg	gct	caa	gtc	aga	2011
Arg	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Ala	Ser	Ala	Val	Ala	Gln	Val	Arg	
500				505					510						515	
ttc	cat	cac	tgt	gac	atg	tat	gga	agt	gct	tgt	gct	gac	tgc	tgc	ctg	2059
Phe	His	His	Cys	Asp	Met	Tyr	Gly	Ser	Ala	Cys	Ala	Asp	Cys	Cys	Leu	
				520				525						530		
gct	cga	gac	cct	tac	tgt	gcc	tgg	gat	ggc	ata	tcc	tgc	tcc	cgg	tat	2107
Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	Gly	Ile	Ser	Cys	Ser	Arg	Tyr	
			535					540						545		



tac cca aca ggc aca cat gca aaa agg cgt ttc cgg aga caa gat gtt Tyr Pro Thr Gly Thr His Ala Lys Arg Arg Phe Arg Arg Gln Asp Val 550 555 560	2155
cga cat gga aat gca gct cag cag tgc ttt gga caa cag ttt gtt ggg Arg His Gly Asn Ala Ala Gln Gln Cys Phe Gly Gln Gln Phe Val Gly 565 570 575	2203
gat gct ttg gat aag act gaa gaa cat ctg gct tat ggc ata gag aac Asp Ala Leu Asp Lys Thr Glu Glu His Leu Ala Tyr Gly Ile Glu Asn 580 585 590 595	2251
aac agt act ttg ctg gaa tgt acc cca cga tct tta caa gcg aaa gtt Asn Ser Thr Leu Glu Cys Thr Pro Arg Ser Leu Gln Ala Lys Val 600 605 610	2299
atc tgg ttt gta cag aaa gga cgt gag aca aga aaa gag gag gtg aag Ile Trp Phe Val Gln Lys Gly Arg Glu Thr Arg Lys Glu Glu Val Lys 615 620 625	2347
aca gat gac aga gtg gtt aag atg gac ctt ggt tta ctc ttc cta agg Thr Asp Asp Arg Val Val Lys Met Asp Leu Gly Leu Leu Phe Leu Arg 630 635 640	2395
tta cac aaa tca gat gct ggg acc tat ttt tgc cag aca gta gag cat Leu His Lys Ser Asp Ala Gly Thr Tyr Phe Cys Gln Thr Val Glu His 645 650 655	2443
agc ttt gtc cat acg gtc cgt aaa atc acc ttg gag gta gtg gaa gag Ser Phe Val His Thr Val Arg Lys Ile Thr Leu Glu Val Val Glu Glu 660 665 670 675	2491
gag aaa gtc gag gat atg ttt aac aag gac gat gag gag gac agg cat Glu Lys Val Glu Asp Met Phe Asn Lys Asp Asp Glu Glu Asp Arg His 680 685 690	2539
cac agg atg cct tgt cct gct cag agt agc atc tcg cag gga gca aaa His Arg Met Pro Cys Pro Ala Gln Ser Ser Ile Ser Gln Gly Ala Lys 695 700 705	2587
cca tgg tac aag gaa ttc ttg cag ctg atc ggt tat agc aac ttc cag Pro Trp Tyr Lys Glu Phe Leu Gln Leu Ile Gly Tyr Ser Asn Phe Gln 710 715 720	2635
aga gtg gaa gaa tac tgc gag aaa gta tgg tgc aca gat aga aag agg Arg Val Glu Glu Tyr Cys Glu Lys Val Trp Cys Thr Asp Arg Lys Arg 725 730 735	2683
aaa aag ctt aaa atg tca ccc tcc aag tgg aag tat gcc aac cct cag Lys Lys Leu Lys Met Ser Pro Ser Lys Trp Lys Tyr Ala Asn Pro Gln 740 745 750 755	2731
gaa aag aag ctc cgt tcc aaa cct gag cat tac cgc ctg ccc agg cac Glu Lys Lys Leu Arg Ser Lys Pro Glu His Tyr Arg Leu Pro Arg His 760 765 770	2779
acg ctg gac tcc tga tggggtgaga ctatctactg tcttttgaag aatttatatt Thr Leu Asp Ser 775	2834
tggaagtaa aaaagtaaaa aaataaatca tccaacttct ttgcattact taaaagagat	2894
ttctgtaata caggaatgac tatgaagggtg ttataataaa ttattctaca tactcatttg	2954

actggataaa	ctttacataa	aattaactaa	ttttttaaat	aatgcattg	cttaatgggt	3014
tctcattatg	tttatcaaaa	aacaactgta	gctgttattt	tcagtacttg	gctgcttttc	3074
tgtgaaaatt	attattttac	ttttggaaga	caagattatt	agaatattga	agaaaaattg	3134
gagacttata	atcatggtaa	atataaaaact	aaatatgttt	taatatttct	gaatttttct	3194
tttccatcac	aatgtaagat	atgcagaata	caagatactt	tggcattctc	atgtgaactt	3254
tctgtactct	ttaaggatta	ttttattagt	gttgtttaag	ccatgagtgt	taagtagcag	3314
gtgtgttg	agtgtgttaa	cccatgaaag	gaaaaatgtc	attctgaggc	ttgtgccctt	3374
cgtaaaaatat	tcattaaagt	acattcacac	tatttttgct	ttataacaca	gtctttaatt	3434
ttcactcact	gtggaaataa	aaactaaggt	aacttctcag	aaagatatca	aatctcagaa	3494
agaatgtcaa	atcagatgaa	gttatagtta	ggattctaac	tactgtaaaa	gatttttgct	3554
tccctcttgt	ggtaaaaaaa	attatattct	cacacatttc	tttttctct	acagacggat	3614
atctgtttag	gaaagatttg	aaagcagatt	atcagtaggt	acatggatac	atcaagttca	3674
tttgcagaaa	caaataactg	aaataaaaaa	catgttaatc	cttgatcat	actttaatat	3734
gaaagtattg	tttatagata	atttatctca	caagtcaaaa	atgaagattt	tgcagcactg	3794
aaaatctatt	aaagctccaa	attttaagtt	tctaaataat	cttcgctgaa	atctaaaata	3854
tactataaca	accgtgtttt	atttgtgaaa	aaaatattaa	agtgatttgc	tctcaaatat	3914
caaattttct	tctctctttt	atattaagag	acagaaaatt	gtttcatgag	ttcacttaac	3974
tactgagata	ttcagagcat	ttttacctct	ctcttaaagt	ttataaaaaa	caattgtatt	4034
tttaagaatg	tttatttatc	aaagtctttc	cttcttctat	taaatattta	gcaattacct	4094
ttctaaaata	tgaaattttg	taagatgttt	tcacctaaat	aaaaattgaa	agcaagtggg	4154
ttacacagga	gaaccattat	gaacatttat	ttagatatta	atcttaaaca	gtgtttattt	4214
cagttttcaa	agttagctta	taggttatat	atttaagtta	aagtgtcat	aatcacttgc	4274
aatttcattg	taaaatgaac	aaatacataa	atattttaag	aaaaatttaa	gtttattcag	4334
ataagtcacc	atgcttcaa	agatctaaga	aatgcaaata	tactgaaaat	tgacatcctc	4394
tgaaaattcc	acttgctatt	taccaagaa	tccactggag	gtcattactg	ccattaaata	4454
ataactgaaa	agactatgta	gtgaaatgta	tttttaaaaa	ctatattcag	taaaagcctg	4514
ctcaatttgg	agaaatagaa	ccacaaacac	agatcacagg	ggccttaca	agtttatgtc	4574
tgaacaaata	agtcaattaa	gtacacttta	ttgaaaattg	ccttccatta	acacacaaga	4634
aagaaagcag	gattttctcc	tgtatctgaa	ttttaaaatt	aaaaaggcag	ataagacata	4694
aatagttatc	attttaattg	caataacaca	gacaagtagt	taatgatgat	aacaatgggtg	4754
taacttgtaa	actaaatatt	tggttaactga	agcaataggc	agaggaaaat	agcttttcta	4814
tgacacaagt	cataagaagt	ccatatactg	aagagcgttt	gattaaaata	aagtgactat	4874

taaccagaaa agaaacattt tacataaaat gctaaaattt attataggaa aataaatcaa 4934  
 acccaaagaa agtttattca atgctaattt gaaagaaaat tgataagaaa actttgaggg 4994  
 cccaagtcca caatttggtg agaccactaa attttacata taattataca cacacatatg 5054  
 tacatatata tgtatataat cttgcttccc gcctgtttat ggcagtactg aagagaaatg 5114  
 ggaaagaaga gggagggaga gagaaagacg aagggagaga gaaagcagtt tccaaggata 5174  
 tgtttcatgt cccaccattt tctcagtttc tccctctctc tcccaacaca cacacacaca 5234  
 caccctcac atactataaa ataaatcttc actgccctat caaaatacaa ataaatcaat 5294  
 ctatgctgtt ctgtccttct tgagaatcta aaacatacca caaaaataca tccccagtct 5354  
 tttgttctgt ctgaggttag aattaattca aattcagaat ctgttgtagg aaatgccag 5414  
 gctttaaaaa ttaaaatgg atggatcttc tctgaactca gggagggcac atacttagat 5474  
 acctacaaga cttggaggaa ttaagagttc acccttcctc tcaccaaatt ttccccattt 5534  
 ttctctttct tgtagaagga gagaaacat gctctctagc aacattgagc aaaaatcata 5594  
 accactcctc taattttctaa gaggcacctc catcgagggc cggctctctg cttctttaga 5654  
 cctcttctat ctttggttaca ggagaggacc tgtggataga cttagttttg acataaaaca 5714  
 atgccccattc acctcctcct tcagcacaac gtcacccatt gggcaagaga tccagatttg 5774  
 ttaacaaaaa agattttact tcgtgattcc acgtctataa ttctatattg ctaatttttt 5834  
 cttttgtgtg aattactgaa tatttcagag caaagctatc aacttgagga aacagggatt 5894  
 aaaaataagg ataaacacta ataagagctc tagaaaaaag ggaacagaaa gtctgcctgt 5954  
 ttagtaagtg gcaattccat acatatttta gagttttttc tatctaaaat tagttaaata 6014  
 cttagaatgt ttgtaatgag tgctcgatat ttgctatagg ttttaggggt ttgtaaactc 6074  
 tcatagtaat tataaacatt tgtaaaattt gtaaaatact ataagtcatt ttgagtgttg 6134  
 gtgttaagca tgaaacaaac agcagctgtt gtccttaaaa atgaattgac ctggccgggc 6194  
 gcgggtggctc acgcctgtaa tcccagcact ttgggaggcc gaggcgggtg gatcatgagg 6254  
 tcaggagatg gagaccatcc tggctaacaa ggtgaaaccc cgtctctact aaaaatacaa 6314  
 aaaattagcc gggcgcggtg gcgggcgcct gtagtcccag ctacttggga ggctgaggca 6374  
 ggagaatggc gtgaaccgga gaagcggagc ttgcagttag ccgagattgc gccactgcag 6434  
 tccgcagtcc ggctgggagc acagagcgag actccgtctc 6474

<210> 16  
 <211> 775  
 <212> PRT  
 <213> Homo sapiens  
 <400> 16

Met Ala Ser Ala Gly His Ile Ile Thr Leu Leu Leu Trp Gly Tyr Leu  
 1 5 10 15  
 Leu Glu Leu Trp Thr Gly Gly His Thr Ala Asp Thr Thr His Pro Arg  
 20 25 30  
 Leu Arg Leu Ser His Lys Glu Leu Leu Asn Leu Asn Arg Thr Ser Ile  
 35 40 45  
 Phe His Ser Pro Phe Gly Phe Leu Asp Leu His Thr Met Leu Leu Asp  
 50 55 60  
 Glu Tyr Gln Glu Arg Leu Phe Val Gly Gly Arg Asp Leu Val Tyr Ser  
 65 70 75 80  
 Leu Ser Leu Glu Arg Ile Ser Asp Gly Tyr Lys Glu Ile His Trp Pro  
 85 90 95  
 Ser Thr Ala Leu Lys Met Glu Glu Cys Ile Met Lys Gly Lys Asp Ala  
 100 105 110  
 Gly Glu Cys Ala Asn Tyr Val Arg Val Leu His His Tyr Asn Arg Thr  
 115 120 125  
 His Leu Leu Thr Cys Gly Thr Gly Ala Phe Asp Pro Val Cys Ala Phe  
 130 135 140  
 Ile Arg Val Gly Tyr His Leu Glu Asp Pro Leu Phe His Leu Glu Ser  
 145 150 155 160  
 Pro Arg Ser Glu Arg Gly Arg Gly Arg Cys Pro Phe Asp Pro Ser Ser  
 165 170 175  
 Ser Phe Ile Ser Thr Leu Ile Gly Ser Glu Leu Phe Ala Gly Leu Tyr  
 180 185 190  
 Ser Asp Tyr Trp Ser Arg Asp Ala Ala Ile Phe Arg Ser Met Gly Arg  
 195 200 205  
 Leu Ala His Ile Arg Thr Glu His Asp Asp Glu Arg Leu Leu Lys Glu  
 210 215 220  
 Pro Lys Phe Val Gly Ser Tyr Met Ile Pro Asp Asn Glu Asp Arg Asp  
 225 230 235 240  
 Asp Asn Lys Val Tyr Phe Phe Phe Thr Glu Lys Ala Leu Glu Ala Glu  
 245 250 255

Asn Asn Ala His Ala Ile Tyr Thr Arg Val Gly Arg Leu Cys Val Asn  
260 265 270

Asp Val Gly Gly Gln Arg Ile Leu Val Asn Lys Trp Ser Thr Phe Leu  
275 280 285

Lys Ala Arg Leu Val Cys Ser Val Pro Gly Met Asn Gly Ile Asp Thr  
290 295 300

Tyr Phe Asp Glu Leu Glu Asp Val Phe Leu Leu Pro Thr Arg Asp His  
305 310 315 320

Lys Asn Pro Val Ile Phe Gly Leu Phe Asn Thr Thr Ser Asn Ile Phe  
325 330 335

Arg Gly His Ala Ile Cys Val Tyr His Met Ser Ser Ile Arg Ala Ala  
340 345 350

Phe Asn Gly Pro Tyr Ala His Lys Glu Gly Pro Glu Tyr His Trp Ser  
355 360 365

Val Tyr Glu Gly Lys Val Pro Tyr Pro Arg Pro Gly Ser Cys Ala Ser  
370 375 380

Lys Val Asn Gly Gly Arg Tyr Gly Thr Thr Lys Asp Tyr Pro Asp Asp  
385 390 395 400

Ala Ile Arg Phe Ala Arg Ser His Pro Leu Met Tyr Gln Ala Ile Lys  
405 410 415

Pro Ala His Lys Lys Pro Ile Leu Val Lys Thr Asp Gly Lys Tyr Asn  
420 425 430

Leu Lys Gln Ile Ala Val Asp Arg Val Glu Ala Glu Asp Gly Gln Tyr  
435 440 445

Asp Val Leu Phe Ile Gly Thr Asp Asn Gly Ile Val Leu Lys Val Ile  
450 455 460

Thr Ile Tyr Asn Gln Glu Met Glu Ser Met Glu Glu Val Ile Leu Glu  
465 470 475 480

Glu Leu Gln Ile Phe Lys Asp Pro Val Pro Ile Ile Ser Met Glu Ile  
485 490 495

Ser Ser Lys Arg Gln Gln Leu Tyr Ile Gly Ser Ala Ser Ala Val Ala  
500 505 510

Gln Val Arg Phe His His Cys Asp Met Tyr Gly Ser Ala Cys Ala Asp  
 515 520 525  
 Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ile Ser Cys  
 530 535 540  
 Ser Arg Tyr Tyr Pro Thr Gly Thr His Ala Lys Arg Arg Phe Arg Arg  
 545 550 555 560  
 Gln Asp Val Arg His Gly Asn Ala Ala Gln Gln Cys Phe Gly Gln Gln  
 565 570 575  
 Phe Val Gly Asp Ala Leu Asp Lys Thr Glu Glu His Leu Ala Tyr Gly  
 580 585 590  
 Ile Glu Asn Asn Ser Thr Leu Leu Glu Cys Thr Pro Arg Ser Leu Gln  
 595 600 605  
 Ala Lys Val Ile Trp Phe Val Gln Lys Gly Arg Glu Thr Arg Lys Glu  
 610 615 620  
 Glu Val Lys Thr Asp Asp Arg Val Val Lys Met Asp Leu Gly Leu Leu  
 625 630 635 640  
 Phe Leu Arg Leu His Lys Ser Asp Ala Gly Thr Tyr Phe Cys Gln Thr  
 645 650 655  
 Val Glu His Ser Phe Val His Thr Val Arg Lys Ile Thr Leu Glu Val  
 660 665 670  
 Val Glu Glu Glu Lys Val Glu Asp Met Phe Asn Lys Asp Asp Glu Glu  
 675 680 685  
 Asp Arg His His Arg Met Pro Cys Pro Ala Gln Ser Ser Ile Ser Gln  
 690 695 700  
 Gly Ala Lys Pro Trp Tyr Lys Glu Phe Leu Gln Leu Ile Gly Tyr Ser  
 705 710 715 720  
 Asn Phe Gln Arg Val Glu Glu Tyr Cys Glu Lys Val Trp Cys Thr Asp  
 725 730 735  
 Arg Lys Arg Lys Lys Leu Lys Met Ser Pro Ser Lys Trp Lys Tyr Ala  
 740 745 750  
 Asn Pro Gln Glu Lys Lys Leu Arg Ser Lys Pro Glu His Tyr Arg Leu  
 755 760 765

Pro Arg His Thr Leu Asp Ser  
770 775

<210> 17  
<211> 2719  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (79)..(2436)

<400> 17  
cgggggcccag gccccgccgc tgcggaagag gtttctagag agtggagcct gcttcctggg 60  
ccctaggccc ctcccaca atg ctt gtc gcc ggt ctt ctt ctc tgg gct tcc 111  
Met Leu Val Ala Gly Leu Leu Leu Trp Ala Ser  
1 5 10  
cta ctg acc ggg gcc tgg cca tcc ttc ccc acc cag gac cac ctc ccg 159  
Leu Leu Thr Gly Ala Trp Pro Ser Phe Pro Thr Gln Asp His Leu Pro  
15 20 25  
gcc acg ccc cgg gtc cgg ctc tca ttc aaa gag ctg aag gcc aca ggc 207  
Ala Thr Pro Arg Val Arg Leu Ser Phe Lys Glu Leu Lys Ala Thr Gly  
30 35 40  
acc gcc cac ttc ttc aac ttc ctg ctc aac aca acc gac tac cga atc 255  
Thr Ala His Phe Phe Asn Phe Leu Leu Asn Thr Thr Asp Tyr Arg Ile  
45 50 55  
ttg ctc aag gac gag gac cac gac cgc atg tac gtg ggc agc aag gac 303  
Leu Leu Lys Asp Glu Asp His Asp Arg Met Tyr Val Gly Ser Lys Asp  
60 65 70 75  
tac gtg ctg tcc ctg gac ctg cac gac atc aac cgc gag ccc ctc att 351  
Tyr Val Leu Ser Leu Asp Leu His Asp Ile Asn Arg Glu Pro Leu Ile  
80 85 90  
ata cac tgg gca gcc tcc cca cag cgc atc gag gaa tgc gtg ctc tca 399  
Ile His Trp Ala Ala Ser Pro Gln Arg Ile Glu Glu Cys Val Leu Ser  
95 100 105  
ggc aag gat gtc aac ggc gag tgt ggg aac ttc gtc agg ctc atc cag 447  
Gly Lys Asp Val Asn Gly Glu Cys Gly Asn Phe Val Arg Leu Ile Gln  
110 115 120  
ccc tgg aac cga aca cac ctg tat gtg tgc ggg aca ggt gcc tac aac 495  
Pro Trp Asn Arg Thr His Leu Tyr Val Cys Gly Thr Gly Ala Tyr Asn  
125 130 135  
ccc atg tgc acc tat gtg aac cgc gga cgc cgc gcc cag gcc aca cca 543  
Pro Met Cys Thr Tyr Val Asn Arg Gly Arg Arg Ala Gln Ala Thr Pro  
140 145 150 155  
tgg acc cag act cag gcg gtc aga ggc cgc ggc agc aga gcc acg gat 591  
Trp Thr Gln Thr Gln Ala Val Arg Gly Arg Gly Ser Arg Ala Thr Asp  
160 165 170  
ggg gcc ctc cgc ccg atg ccc aca gcc cca cgc cag gat tac atc ttc 639  
Gly Ala Leu Arg Pro Met Pro Thr Ala Pro Arg Gln Asp Tyr Ile Phe  
175 180 185

tac ctg gag cct gag cga ctc gag tca ggg aag ggc aag tgt ccg tac	687
Tyr Leu Glu Pro Glu Arg Leu Glu Ser Gly Lys Gly Lys Cys Pro Tyr	
190 195 200	
gat ccc aag ctg gac aca gca tcg gcc ctc atc aat gag gag ctc tat	735
Asp Pro Lys Leu Asp Thr Ala Ser Ala Leu Ile Asn Glu Glu Leu Tyr	
205 210 215	
gct ggt gtg tac atc gat ttt atg ggc act gat gca gcc atc ttc cgc	783
Ala Gly Val Tyr Ile Asp Phe Met Gly Thr Asp Ala Ala Ile Phe Arg	
220 225 230 235	
aca ctt gga aag cag aca gcc atg cgc acg gat cag tac aac tcc cgg	831
Thr Leu Gly Lys Gln Thr Ala Met Arg Thr Asp Gln Tyr Asn Ser Arg	
240 245 250	
tgg ctg aac gac ccg tcg ttc atc cat gct gag ctc att cct gac agt	879
Trp Leu Asn Asp Pro Ser Phe Ile His Ala Glu Leu Ile Pro Asp Ser	
255 260 265	
gcg gag cgc aat gat gat aag ctt tac ttc ttc ttc cgt gag cgg tcg	927
Ala Glu Arg Asn Asp Asp Lys Leu Tyr Phe Phe Phe Arg Glu Arg Ser	
270 275 280	
gca gag gcg ccg cag agc ccc gcg gtg tac gcc cgc atc ggg cgc att	975
Ala Glu Ala Pro Gln Ser Pro Ala Val Tyr Ala Arg Ile Gly Arg Ile	
285 290 295	
tgc ctg aac gat gac ggt ggt cac tgt tgc ctg gtc aac aag tgg agc	1023
Cys Leu Asn Asp Asp Gly Gly His Cys Cys Leu Val Asn Lys Trp Ser	
300 305 310 315	
aca ttc ctg aag gcg cgg ctc gtc tgc tct gtc ccg ggc gag gat ggc	1071
Thr Phe Leu Lys Ala Arg Leu Val Cys Ser Val Pro Gly Glu Asp Gly	
320 325 330	
att gag act cac ttt gat gag ctc cag gac gtg ttt gtc cag cag acc	1119
Ile Glu Thr His Phe Asp Glu Leu Gln Asp Val Phe Val Gln Gln Thr	
335 340 345	
cag gac gtg agg aac cct gtc att tac gct gtc ttt acc tcc tct ggc	1167
Gln Asp Val Arg Asn Pro Val Ile Tyr Ala Val Phe Thr Ser Ser Gly	
350 355 360	
tcc gtg ttc cga ggc tct gcc gtg tgt gtc tac tcc atg gct gat att	1215
Ser Val Phe Arg Gly Ser Ala Val Cys Val Tyr Ser Met Ala Asp Ile	
365 370 375	
cgc atg gtc ttc aac ggg ccc ttt gcc cac aaa gag ggg ccc aac tac	1263
Arg Met Val Phe Asn Gly Pro Phe Ala His Lys Glu Gly Pro Asn Tyr	
380 385 390 395	
cag tgg atg ccc ttc tca ggg aag atg ccc tac cca cgg ccg ggc acg	1311
Gln Trp Met Pro Phe Ser Gly Lys Met Pro Tyr Pro Arg Pro Gly Thr	
400 405 410	
tgc cct ggt gga acc ttc acg cca tct atg aag tcc acc aag gat tat	1359
Cys Pro Gly Gly Thr Phe Thr Pro Ser Met Lys Ser Thr Lys Asp Tyr	
415 420 425	
cct gat gag gtg atc aac ttc atg cgc agc cac cca ctc atg tac cag	1407
Pro Asp Glu Val Ile Asn Phe Met Arg Ser His Pro Leu Met Tyr Gln	
430 435 440	



gcc gtg tac cct ctg cag cgg cgg ccc ctg gta gtc cgc aca ggt gct Ala Val Tyr Pro Leu Gln Arg Arg Pro Leu Val Val Arg Thr Gly Ala 445 450 455	1455
ccc tac cgc ctt acc act att gcc gtg gac cag gtg gat gca ggc gac Pro Tyr Arg Leu Thr Thr Ile Ala Val Asp Gln Val Asp Ala Gly Asp 460 465 470 475	1503
ggg cgc tat gag gtg ctt ttc ctg ggc aca gac cgc ggg aca gtg cag Gly Arg Tyr Glu Val Leu Phe Leu Gly Thr Asp Arg Gly Thr Val Gln 480 485 490	1551
aag gtc att gtg ctg ccc aag gat gac cag gag atg gag gag ctc atg Lys Val Ile Val Leu Pro Lys Asp Asp Gln Glu Met Glu Glu Leu Met 495 500 505	1599
ctg gag gag gtg gag gtc ttc aag gat cca gca ccc gtc aag acc atg Leu Glu Glu Val Glu Val Phe Lys Asp Pro Ala Pro Val Lys Thr Met 510 515 520	1647
acc atc tct tct aag agg caa caa ctc tac gtg gcg tca gcc gtg ggt Thr Ile Ser Ser Lys Arg Gln Gln Leu Tyr Val Ala Ser Ala Val Gly 525 530 535	1695
gtc aca cac ctg agc ctg cac cgc tgc cag gcg tat ggg gct gcc tgt Val Thr His Leu Ser Leu His Arg Cys Gln Ala Tyr Gly Ala Ala Cys 540 545 550 555	1743
gct gac tgc tgc ctt gcc cgg gac cct tac tgt gcc tgg gat ggc cag Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Gln 560 565 570	1791
gcc tgc tcc cgc tat aca gca tcc tcc aag agg cgg agc cgc cgg cag Ala Cys Ser Arg Tyr Thr Ala Ser Ser Lys Arg Arg Ser Arg Arg Gln 575 580 585	1839
gac gtc cgg cac gga aac ccc atc agg cag tgc cgt ggg ttc aac tcc Asp Val Arg His Gly Asn Pro Ile Arg Gln Cys Arg Gly Phe Asn Ser 590 595 600	1887
aat gcc aac aag aat gcc gtg gag tct gtg cag tat ggc gtg gcc ggc Asn Ala Asn Lys Asn Ala Val Glu Ser Val Gln Tyr Gly Val Ala Gly 605 610 615	1935
agc gca gcc ttc ctt gag tgc cag ccc cgc tgc ccc caa gcc act gtt Ser Ala Ala Phe Leu Glu Cys Gln Pro Arg Ser Pro Gln Ala Thr Val 620 625 630 635	1983
aag tgg ctg ttc cag cga gat cct ggt gac cgg cgc cga gag att cgt Lys Trp Leu Phe Gln Arg Asp Pro Gly Asp Arg Arg Arg Glu Ile Arg 640 645 650	2031
gca gag gac cgc ttc ctg cgc aca gag cag ggc ttg ttg ctc cgt gca Ala Glu Asp Arg Phe Leu Arg Thr Glu Gln Gly Leu Leu Leu Arg Ala 655 660 665	2079
ctg cag ctc agc gat cgt ggc ctc tac tcc tgc aca gcc act gag aac Leu Gln Leu Ser Asp Arg Gly Leu Tyr Ser Cys Thr Ala Thr Glu Asn 670 675 680	2127
aac ttt aag cac gtc gtc aca cga gtg cag ctg cat gta ctg ggc cgg Asn Phe Lys His Val Val Thr Arg Val Gln Leu His Val Leu Gly Arg 685 690 695	2175

gac gcc gtc cat gct gcc ctc ttc cca cca ctg tcc atg agc gcc ccg 2223  
 Asp Ala Val His Ala Ala Leu Phe Pro Pro Leu Ser Met Ser Ala Pro  
 700 705 710 715

cca ccc cca ggc gca ggc ccc cca acg cct cct tac cag gag tta gcc 2271  
 Pro Pro Pro Gly Ala Gly Pro Pro Thr Pro Pro Tyr Gln Glu Leu Ala  
 720 725 730

cag ctg ctg gcc cag cca gaa gtg ggc ctc atc cac cag tac tgc cag 2319  
 Gln Leu Leu Ala Gln Pro Glu Val Gly Leu Ile His Gln Tyr Cys Gln  
 735 740 745

ggt tac tgg cgc cat gtg ccc ccc agc ccc agg gag gct cca ggg gca 2367  
 Gly Tyr Trp Arg His Val Pro Pro Ser Pro Arg Glu Ala Pro Gly Ala  
 750 755 760

ccc cgg tct cct gag ccc cag gac cag aaa aag ccc cgg aac cgc cgg 2415  
 Pro Arg Ser Pro Glu Pro Gln Asp Gln Lys Lys Pro Arg Asn Arg Arg  
 765 770 775

cac cac cct ccg gac aca tga ggccagctgc ctgtgcctgc catgggccag 2466  
 His His Pro Pro Asp Thr  
 780 785

gctaggcctt ggtccctttt aatataaaag atatatatat atatatatat atatattaaa 2526  
 atatcgggggt ggggggtgat tggaaggag ggaggtggcc ttcccaatgc gcgttattcg 2586  
 gggttattga agaataatat tgcaagtgac agccagaagt agactttctg tcctcacacc 2646  
 gaagaacccg agtgagcagg agggagggag agacgcgaag agaccttttt tcctttttgg 2706  
 agaccttgtc cgc 2719

<210> 18  
 <211> 785  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Met Leu Val Ala Gly Leu Leu Leu Trp Ala Ser Leu Leu Thr Gly Ala  
 1 5 10 15

Trp Pro Ser Phe Pro Thr Gln Asp His Leu Pro Ala Thr Pro Arg Val  
 20 25 30

Arg Leu Ser Phe Lys Glu Leu Lys Ala Thr Gly Thr Ala His Phe Phe  
 35 40 45

Asn Phe Leu Leu Asn Thr Thr Asp Tyr Arg Ile Leu Leu Lys Asp Glu  
 50 55 60

Asp His Asp Arg Met Tyr Val Gly Ser Lys Asp Tyr Val Leu Ser Leu  
 65 70 75 80

Asp Leu His Asp Ile Asn Arg Glu Pro Leu Ile Ile His Trp Ala Ala  
 85 90 95  
 Ser Pro Gln Arg Ile Glu Glu Cys Val Leu Ser Gly Lys Asp Val Asn  
 100 105 110  
 Gly Glu Cys Gly Asn Phe Val Arg Leu Ile Gln Pro Trp Asn Arg Thr  
 115 120 125  
 His Leu Tyr Val Cys Gly Thr Gly Ala Tyr Asn Pro Met Cys Thr Tyr  
 130 135 140  
 Val Asn Arg Gly Arg Arg Ala Gln Ala Thr Pro Trp Thr Gln Thr Gln  
 145 150 155 160  
 Ala Val Arg Gly Arg Gly Ser Arg Ala Thr Asp Gly Ala Leu Arg Pro  
 165 170 175  
 Met Pro Thr Ala Pro Arg Gln Asp Tyr Ile Phe Tyr Leu Glu Pro Glu  
 180 185 190  
 Arg Leu Glu Ser Gly Lys Gly Lys Cys Pro Tyr Asp Pro Lys Leu Asp  
 195 200 205  
 Thr Ala Ser Ala Leu Ile Asn Glu Glu Leu Tyr Ala Gly Val Tyr Ile  
 210 215 220  
 Asp Phe Met Gly Thr Asp Ala Ala Ile Phe Arg Thr Leu Gly Lys Gln  
 225 230 235 240  
 Thr Ala Met Arg Thr Asp Gln Tyr Asn Ser Arg Trp Leu Asn Asp Pro  
 245 250 255  
 Ser Phe Ile His Ala Glu Leu Ile Pro Asp Ser Ala Glu Arg Asn Asp  
 260 265 270  
 Asp Lys Leu Tyr Phe Phe Phe Arg Glu Arg Ser Ala Glu Ala Pro Gln  
 275 280 285  
 Ser Pro Ala Val Tyr Ala Arg Ile Gly Arg Ile Cys Leu Asn Asp Asp  
 290 295 300  
 Gly Gly His Cys Cys Leu Val Asn Lys Trp Ser Thr Phe Leu Lys Ala  
 305 310 315 320  
 Arg Leu Val Cys Ser Val Pro Gly Glu Asp Gly Ile Glu Thr His Phe  
 325 330 335

Asp Glu Leu Gln Asp Val Phe Val Gln Gln Thr Gln Asp Val Arg Asn  
 340 345 350

Pro Val Ile Tyr Ala Val Phe Thr Ser Ser Gly Ser Val Phe Arg Gly  
 355 360 365

Ser Ala Val Cys Val Tyr Ser Met Ala Asp Ile Arg Met Val Phe Asn  
 370 375 380

Gly Pro Phe Ala His Lys Glu Gly Pro Asn Tyr Gln Trp Met Pro Phe  
 385 390 395 400

Ser Gly Lys Met Pro Tyr Pro Arg Pro Gly Thr Cys Pro Gly Gly Thr  
 405 410 415

Phe Thr Pro Ser Met Lys Ser Thr Lys Asp Tyr Pro Asp Glu Val Ile  
 420 425 430

Asn Phe Met Arg Ser His Pro Leu Met Tyr Gln Ala Val Tyr Pro Leu  
 435 440 445

Gln Arg Arg Pro Leu Val Val Arg Thr Gly Ala Pro Tyr Arg Leu Thr  
 450 455 460

Thr Ile Ala Val Asp Gln Val Asp Ala Gly Asp Gly Arg Tyr Glu Val  
 465 470 475 480

Leu Phe Leu Gly Thr Asp Arg Gly Thr Val Gln Lys Val Ile Val Leu  
 485 490 495

Pro Lys Asp Asp Gln Glu Met Glu Glu Leu Met Leu Glu Glu Val Glu  
 500 505 510

Val Phe Lys Asp Pro Ala Pro Val Lys Thr Met Thr Ile Ser Ser Lys  
 515 520 525

Arg Gln Gln Leu Tyr Val Ala Ser Ala Val Gly Val Thr His Leu Ser  
 530 535 540

Leu His Arg Cys Gln Ala Tyr Gly Ala Ala Cys Ala Asp Cys Cys Leu  
 545 550 555 560

Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Gln Ala Cys Ser Arg Tyr  
 565 570 575

Thr Ala Ser Ser Lys Arg Arg Ser Arg Arg Gln Asp Val Arg His Gly  
 580 585 590

Asn Pro Ile Arg Gln Cys Arg Gly Phe Asn Ser Asn Ala Asn Lys Asn  
595 600 605

Ala Val Glu Ser Val Gln Tyr Gly Val Ala Gly Ser Ala Ala Phe Leu  
610 615 620

Glu Cys Gln Pro Arg Ser Pro Gln Ala Thr Val Lys Trp Leu Phe Gln  
625 630 635 640

Arg Asp Pro Gly Asp Arg Arg Arg Glu Ile Arg Ala Glu Asp Arg Phe  
645 650 655

Leu Arg Thr Glu Gln Gly Leu Leu Leu Arg Ala Leu Gln Leu Ser Asp  
660 665 670

Arg Gly Leu Tyr Ser Cys Thr Ala Thr Glu Asn Asn Phe Lys His Val  
675 680 685

Val Thr Arg Val Gln Leu His Val Leu Gly Arg Asp Ala Val His Ala  
690 695 700

Ala Leu Phe Pro Pro Leu Ser Met Ser Ala Pro Pro Pro Gly Ala  
705 710 715 720

Gly Pro Pro Thr Pro Pro Tyr Gln Glu Leu Ala Gln Leu Leu Ala Gln  
725 730 735

Pro Glu Val Gly Leu Ile His Gln Tyr Cys Gln Gly Tyr Trp Arg His  
740 745 750

Val Pro Pro Ser Pro Arg Glu Ala Pro Gly Ala Pro Arg Ser Pro Glu  
755 760 765

Pro Gln Asp Gln Lys Lys Pro Arg Asn Arg Arg His His Pro Pro Asp  
770 775 780

Thr  
785

<210> 19  
<211> 649  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (17) .. (592)

```

<220>
<221> misc_feature
<222> (17)..(94)
<223> Signal peptide

<400> . 19
tcgggcctcc gaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc ctt      52
      Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
            1             5             10

gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc      100
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
      15             20             25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg      148
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
      30             35             40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac      196
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
      45             50             55

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc      244
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
            65             70             75

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg      292
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
            80             85             90

gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg      340
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
            95             100            105

atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag      388
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
            110            115            120

cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa      436
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
            125            130            135            140

aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa      484
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
            145            150            155

gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc      532
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
            160            165            170

aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag      580
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
            175            180            185

ccg agg cgg tga gccgggcagg aggaaggagc ctccctcagc gtttcgggaa      632
Pro Arg Arg
            190

ccagatctct caccagg      649

```

<210> 20  
 <211> 191  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (17)..(94)  
 <223> Signal peptide

<400> 20

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly  
 130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr  
 145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln  
 165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg  
 180 185 190

<210> 21  
 <211> 755  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5) .. (628)

&lt;400&gt; 21

cacc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag	49
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln	
1 5 10 15	
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac	97
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His	
20 25 30	
cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc	145
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys	
35 40 45	
cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc	193
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr	
50 55 60	
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt	241
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly	
65 70 75	
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac	289
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His	
80 85 90 95	
caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg	337
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu	
100 105 110	
ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa	385
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys	
115 120 125	
aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac	433
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His	
130 135 140	
cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca	481
Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala	
145 150 155	
ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct	529
Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser	
160 165 170 175	
gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc	577
Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala	
180 185 190	
gcc gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct	625
Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala	
195 200 205	
tag agctcaaccc agacacctgc aggtgccgga agctgcgaag gtgacacatg	678
gcttttcaga ctcagcaggg tgacttgct cagaggctat atcccagtgg gggaacaaag	738



aggagcctgg taaaaaa

755

<210> 22  
 <211> 207  
 <212> PRT  
 <213> Homo sapiens

<400> 22

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
 1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
 20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
 35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
 50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
 100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg  
 130 135 140

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro  
 145 150 155 160

Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala  
 165 170 175

His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala  
 180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala  
 195 200 205

[illegible]

gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt	837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys	
150 155 160	
ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg	885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr	
165 170 175	
agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa	933
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln	
180 185 190	
ggc ccc aaa cca gta aca atc agt ttt gcc aat cac act tcc tgc cga	981
Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	
195 200 205 210	
tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga	1029
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg	
215 220 225	
cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc	1077
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr	
230 235 240	
tgc ccc acc aat tac atg tgg aat aat cac atc tgc aga tgc ctg gct	1125
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala	
245 250 255	
cag gaa gat ttt atg ttt tcc tgc gat gct gga gat gac tca aca gat	1173
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp	
260 265 270	
gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc	1221
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr	
275 280 285 290	
tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct gcc agc tgt gga ccc	1269
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro	
295 300 305	
cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa	1317
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys	
310 315 320	
ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca	1365
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr	
325 330 335	
tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat	1413
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn	
340 345 350	
cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg	1461
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu	
355 360 365 370	
tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg	1509
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg	
375 380 385	
cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt	1557
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser	
390 395 400	

caaaatatgt ttaaaataaa atgaaaattg tattat 1997

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe  
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr  
 145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr  
 165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu  
 180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser  
 195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile  
 210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn  
 225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys  
 245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser  
 260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu  
 275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys  
 290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys  
 305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu  
 325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro  
 340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys  
 355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr  
 370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser  
 385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro  
 405 410 415

Gln Met Ser

<210> 25  
 <211> 2029  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (411)..(1475)

<400> 25  
 gttgggttcc agctttctgt agctgtaagc attgggtggcc acaccacctc cttacaaagc 60  
 aactagaacc tgcggcatac attggagaga tttttttaat tttctggaca tgaagtaa 120  
 ttagagtgtt ttctaatttc aggtagaaga catgtccacc ttctgattat ttttggagaa 180  
 cattttgatt tttttcatct ctctctcccc acccctaaga ttgtgcaaaa aaagcgtacc 240  
 ttgcctaatt gaaataattt cattggattt tgatcagaac tgattatttg gttttctgtg 300  
 tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta 360  
 gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac 416  
 Met Tyr  
 1  
 aga gag tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg 464  
 Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu  
 5 10 15  
 gtg cag ggc tcc agt aat gaa cat gga cca gtg aag cga tca tct cag 512  
 Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln  
 20 25 30  
 tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg 560  
 Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu  
 35 40 45 50  
 gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga 608  
 Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg  
 55 60 65  
 tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca 656  
 Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala  
 70 75 80  
 tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca 704  
 Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr  
 85 90 95  
 cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga 752  
 Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg  
 100 105 110  
 gaa acg tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca 800  
 Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr  
 115 120 125 130

ttc ttc aag ccc cct tgt gtg aac gtg ttc cga tgt ggt ggc tgt tgc	848
Phe Phe Lys Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys	
135 140 145	
aat gaa gag agc ctt atc tgt atg aac acc agc acc tcg tac att tcc	896
Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr Ile Ser	
150 155 160	
aaa cag ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta	944
Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu	
165 170 175	
gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca	992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr	
180 185 190	
gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct	1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro	
195 200 205 210	
gaa gaa gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg	1088
Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met	
215 220 225	
cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca	1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro	
230 235 240	
ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt	1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys	
245 250 255	
ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa	1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys	
260 265 270	
aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc	1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys	
275 280 285 290	
ttt gag tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta	1328
Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu	
295 300 305	
ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc	1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr	
310 315 320	
aga cca tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt	1424
Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe	
325 330 335	
cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct	1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro	
340 345 350	
tga ttcagcgttc caagttcccc atccctgtca tttttaacag catgctgctt	1525
tgccaagttg ctgtcactgt ttttttccca ggtgttaaaa aaaaaatcca ttttacacag	1585
caccacagtg aatccagacc aaccttccat tcacaccagc taaggagtcc ctgggttcatt	1645

```

gatggatgtc ttctagctgc agatgcctct gcgcaccaag gaatggagag gaggggaccc 1705
atgtaatcct tttgtttagt tttgtttttg ttttttggtg aatgagaaag gtgtgctggt 1765
catggaatgg caggtgtcat atgactgatt actcagagca gatgaggaaa actgtagtct 1825
ctgagtcctt tgctaatcgc aactcttctg aattattctg attctttttt atgcagaatt 1885
tgattcgtat gatcagtact gactttctga ttactgtcca gcttatagtc ttccagttta 1945
atgaactacc atctgatgtt tcatatttaa gtgtatttaa agaaaataaa caccattatt 2005
caagccaaaa aaaaaaaaaa aaaa 2029

```

&lt;210&gt; 26

&lt;211&gt; 354

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

```

Met Tyr Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val
1          5          10          15

```

```

Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser
20          25          30

```

```

Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
35          40          45

```

```

Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
50          55          60

```

```

Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65          70          75          80

```

```

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85          90          95

```

```

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100          105          110

```

```

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115          120          125

```

```

Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
130          135          140

```

```

Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145          150          155          160

```



Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro  
 165 170 175

Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu  
 180 185 190

Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln  
 195 200 205

Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile  
 210 215 220

Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu  
 225 230 235 240

Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala  
 245 250 255

Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val  
 260 265 270

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys  
 275 280 285

Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His  
 290 295 300

Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe  
 305 310 315 320

His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys  
 325 330 335

Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys  
 340 345 350

Asn Pro

<210> 27  
 <211> 1645  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (322)..(771)

<400> 27  
 gggattcggg ccgcccagct acgggaggac ctggagtggc actgggcgcc cgacggacca 60

tccccggggac ccgcctgccc ctcggcgccc cgccccgccc ggccgctccc cgtcgggttc	120
cccagccaca gccttaccta cgggctcctg actccgcaag gcttccagaa gatgctcgaa	180
ccaccgggccc gggcctcggg gcagcagtga gggaggcgctc cagcccccca ctcagctctt	240
ctcctcctgt gccaggggct ccccggggga tgagcatggg ggttttccct cggagcccc	300
tggctcggga cgtctgagaa g atg ccg gtc atg agg ctg ttc cct tgc ttc	351
Met Pro Val Met Arg Leu Phe Pro Cys Phe	
1 5 10	
ctg cag ctc ctg gcc ggg ctg gcg ctg cct gct gtg ccc ccc cag cag	399
Leu Gln Leu Leu Ala Gly Leu Ala Leu Pro Ala Val Pro Pro Gln Gln	
15 20 25	
tgg gcc ttg tct gct ggg aac ggc tgc tca gag gtg gaa gtg gta ccc	447
Trp Ala Leu Ser Ala Gly Asn Gly Ser Ser Glu Val Glu Val Val Pro	
30 35 40	
ttc cag gaa gtg tgg ggc cgc agc tac tgc cgg gcg ctg gag agg ctg	495
Phe Gln Glu Val Trp Gly Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu	
45 50 55	
gtg gac gtc gtg tcc gag tac ccc agc gag gtg gag cac atg ttc agc	543
Val Asp Val Val Ser Glu Tyr Pro Ser Glu Val Glu His Met Phe Ser	
60 65 70	
cca tcc tgt gtc tcc ctg ctg cgc tgc acc ggc tgc tgc ggc gat gag	591
Pro Ser Cys Val Ser Leu Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu	
75 80 85 90	
aat ctg cac tgt gtg ccg gtg gag acg gcc aat gtc acc atg cag ctc	639
Asn Leu His Cys Val Pro Val Glu Thr Ala Asn Val Thr Met Gln Leu	
95 100 105	
cta aag atc cgt tct ggg gac cgg ccc tcc tac gtg gag ctg acg ttc	687
Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe	
110 115 120	
tct cag cac gtt cgc tgc gaa tgc cgg cct ctg cgg gag aag atg aag	735
Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu Lys Met Lys	
125 130 135	
ccg gaa agg tgc ggc gat gct gtt ccc cgg agg taa cccaccctt	781
Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg	
140 145	
ggaggagaga gaccccgcac ccggctcgtg tatttattac cgtcacactc ttcagtgact	841
cctgctggta cctgccctct atttattagc caactgtttc cctgctgaat gcctcgctcc	901
cttcaagacg aggggcaggg aaggacagga ccctcaggaa ttcagtgcct tcaacaacgt	961
gagagaaaga gagaagccag ccacagaccc ctgggagctt ccgctttgaa agaagcaaga	1021
cacgtggcct cgtgaggggc aagctaggcc ccagaggccc tggaggtctc caggggcctg	1081
cagaaggaaa gaagggggcc ctgctacctg ttcttgggcc tcaggctctg cacagacaag	1141
cagcccttgc ttctggagct cctgtccaaa gtagggatgc ggattctgct ggggccgcca	1201

cggcctggtg gtgggaaggc cggcagcggg cggaggggat tcagccactt cccctcttc 1261  
 ttctgaagat cagaacattc agctctggag aacagtgggt gcctgggggc ttttgccact 1321  
 ccttgctccc cgtgatctcc cctcacactt tgccatttgc ttgtactggg acattgttct 1381  
 ttccggccga ggtgccacca ccctgcccc actaagagac acatacagag tgggccccgg 1441  
 gctggagaaa gagctgcctg gatgagaaac agctcagcca gtggggatga ggtcaccagg 1501  
 ggaggagcct gtgcgtccca gctgaaggca gtggcagggg agcaggttcc ccaagggccc 1561  
 tggcaccccc acaagctgtc cctgcagggc catctgactg ccaagccaga ttctcttgaa 1621  
 taaagtattc tagtgtggaa acgc 1645

&lt;210&gt; 28

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Homo. sapiens

&lt;400&gt; 28

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly  
 1 5 10 15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly  
 20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly  
 35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu  
 50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu  
 65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro  
 85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly  
 100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys  
 115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Cys Gly Asp  
 130 135 140

Ala Val Pro Arg Arg  
 145

<210> 29  
 <211> 4230  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(4065)

<400> 29  
 agc aag gtg ctg ctg gcc gtc gcc ctg tgg ctc tgc gtg gag acc cgg 48  
 Ser Lys Val Leu Ala Val Ala Leu Trp Leu Cys Val Glu Thr Arg  
 1 5 10 15  
 gcc gcc tct gtg ggt ttg cct agt gtt tct ctt gat ctg ccc agg ctc 96  
 Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro Arg Leu  
 20 25 30  
 agc ata caa aaa gac ata ctt aca att aag gct aat aca act ctt caa 144  
 Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr Leu Gln  
 35 40 45  
 att act tgc agg gga cag agg gac ttg gac tgg ctt tgg ccc aat aat 192  
 Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Asn  
 50 55 60  
 cag agt ggc agt gag caa agg gtg gag gtg act gag tgc agc gat ggc 240  
 Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser Asp Gly  
 65 70 75 80  
 ctc ttc tgt aag aca ctc aca att cca aaa gtg atc gga aat gac act 288  
 Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn Asp Thr  
 85 90 95  
 gga gcc tac aag tgc ttc tac cgg gaa act gac ttg gcc tcg gtc att 336  
 Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser Val Ile  
 100 105 110  
 tat gtc tat gtt caa gat tac aga tct cca ttt att gct tct gtt agt 384  
 Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser  
 115 120 125  
 gac caa cat gga gtc gtg tac att act gag aac aaa aac aaa act gtg 432  
 Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val  
 130 135 140  
 gtg att cca tgt ctc ggg tcc att tca aat ctc aac gtg tca ctt tgt 480  
 Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys  
 145 150 155 160  
 gca aga tac cca gaa aag aga ttt gtt cct gat ggt aac aga att tcc 528  
 Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser  
 165 170 175  
 tgg gac agc aag aag ggc ttt act att ccc agc tac atg atc agc tat 576  
 Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile Ser Tyr  
 180 185 190  
 gct ggc atg gtc ttc tgt gaa gca aaa att aat gat gaa agt tac cag 624  
 Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser Tyr Gln  
 195 200 205

tct att atg tac ata gtt gtc gtt gta ggg tat agg att tat gat gtg Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp Val 210 215 220	672
gtt ctg agt ccg tct cat gga att gaa cta tct gtt gga gaa aag ctt Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu 225 230 235 240	720
gtc tta aat tgt aca gca aga act gaa cta aat gtg ggg att gac ttc Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe 245 250 255	768
aac tgg gaa tac cct tct tcg aag cat cag cat aag aaa ctt gta aac Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn 260 265 270	816
cga gac cta aaa acc cag tct ggg agt gag atg aag aaa ttt ttg agc Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser 275 280 285	864
acc tta act ata gat ggt gta acc cgg agt gac caa gga ttg tac acc Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr 290 295 300	912
tgt gca gca tcc agt ggg ctg atg acc aag aag aac agc aca ttt gtc Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val 305 310 315 320	960
agg gtc cat gaa aaa cct ttt gtt gct ttt gga agt ggc atg gaa tct Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met Glu Ser 325 330 335	1008
ctg gtg gaa gcc acg gtg ggg gag cgt gtc aga atc cct gcg aag tac Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala Lys Tyr 340 345 350	1056
ctt ggt tac cca ccc cca gaa ata aaa tgg tat aaa aat gga ata ccc Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly Ile Pro 355 360 365	1104
ctt gag tcc aat cac aca att aaa gcg ggg cat gta ctg acg att atg Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr Ile Met 370 375 380	1152
gaa gtg agt gaa aga gac aca gga aat tac act gtc atc ctt acc aat Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu Thr Asn 385 390 395 400	1200
ccc att tca aag gag aag cag agc cat gtg gtc tct ctg gtt gtg tat Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val Val Tyr 405 410 415	1248
gtc cca ccc cag att ggt gag aaa tct cta atc tct cct gtg gat tcc Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val Asp Ser 420 425 430	1296
tac cag tac ggc acc act caa acg ctg aca tgt acg gtc tat gcc att Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr Ala Ile 435 440 445	1344
cct ccc ccg cat cac atc cac tgg tat tgg cag ttg gag gaa gag tgc Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu Glu Cys 450 455 460	1392

gcc aac gag ccc agc caa gct gtc tca gtg aca aac cca tac cct tgt Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr Pro Cys 465 470 475 480	1440
gaa gaa tgg aga agt gtg gag gac ttc cag gga gga aat aaa att gaa Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu 485 490 495	1488
gtt aat aaa aat caa ttt gct cta att gaa gga aaa aac aaa act gta Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys Thr Val 500 505 510	1536
agt acc ctt gtt atc caa gcg gca aat gtg tca gct ttg tac aaa tgt Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys 515 520 525	1584
gaa gcg gtc aac aaa gtc ggg aga gga gag agg gtg atc tcc ttc cac Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser Phe His 530 535 540	1632
gtg acc agg ggt cct gaa att act ttg caa cct gac atg cag ccc act Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln Pro Thr 545 550 555 560	1680
gag cag gag agc gtg tct ttg tgg tgc act gca gac aga tct acg ttt Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser Thr Phe 565 570 575	1728
gag aac ctc aca tgg tac aag ctt ggc cca cag cct ctg cca atc cat Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro Ile His 580 585 590	1776
gtg gga gag ttg ccc aca cct gtt tgc aag aac ttg gat act ctt tgg Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr Leu Trp 595 600 605	1824
aaa ttg aat gcc acc atg ttc tct aat agc aca aat gac att ttg atc Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile 610 615 620	1872
atg gag ctt aag aat gca tcc ttg cag gac caa gga gac tat gtc tgc Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys 625 630 635 640	1920
ctt gct caa gac agg aag acc aag aaa aga cat tgc gtg gtc agg cag Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val Arg Gln 645 650 655	1968
ctc aca gtc cta gag cgt gtg gca ccc acg atc aca gga aac ctg gag Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn Leu Glu 660 665 670	2016
aat cag acg aca agt att ggg gaa agc atc gaa gtc tca tgc acg gca Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys Thr Ala 675 680 685	2064
tct ggg aat ccc cct cca cag atc atg ttg ttt aaa gat aat gag acc Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn Glu Thr 690 695 700	2112
ctt gta gaa gac tca ggc att gta ttg aag gat ggg aac cgg aac ctc Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg Asn Leu 705 710 715 720	2160

act atc cgc aga gtg agg aag gag gac gaa ggc ctc tac acc tgc cag Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr Cys Gln 725 730 735	2208
gca tgc agt gtt ctt ggc tgt gca aaa gtg gag gca ttt ttc ata ata Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe Ile Ile 740 745 750	2256
gaa ggt gcc cag gaa aag acg aac ttg gaa atc att att cta gta ggc Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu Val Gly 755 760 765	2304
acg acg gtg att gcc atg ttc ttc tgg cta ctt ctt gtc atc atc cta Thr Thr Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Ile Leu 770 775 780	2352
ggg acc gtt aag cgg gcc aat gga ggg gaa ctg aag aca ggc tac ttg Gly Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly Tyr Leu 785 790 795 800	2400
tcc atc gtc atg gat cca gat gaa ctc cca ttg gat gaa cat tgt gaa Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His Cys Glu 805 810 815	2448
cga ctg cct tat gat gcc agc aaa tgg gaa ttc ccc aga gac cgg ctg Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu 820 825 830	2496
aac cta ggt aag cct ctt ggc cgt ggt gcc ttt ggc caa gag att gaa Asn Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Glu Ile Glu 835 840 845	2544
gca gat gcc ttt gga att gac aag aca gca act tgc agg aca gta gca Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr Val Ala 850 855 860	2592
gtc aaa atg ttg aaa gaa gga gca aca cac agt gag cat cga gct ctc Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu 865 870 875 880	2640
atg tct gaa ctc aag atc ctc att cat att ggt cac cat ctc aat gtg Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val 885 890 895	2688
gtc aac ctt cta ggt gcc tgt acc aag cca gga ggg cca ctc atg gtg Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val 900 905 910	2736
att gtg gaa ttc tgc aaa ttt gga aac ctg tcc act tac ctg agg agc Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Ser 915 920 925	2784
aag aga aat gaa ttt gtc ccc tac aag acc aaa ggg gca cga ttc cgt Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg Phe Arg 930 935 940	2832
caa ggg aaa gac tac gtt gga gca atc cct gtg gat ctg aaa cgg cgc Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys Arg Arg 945 950 955 960	2880
ttg gac agc atc acc agt agc cag agc tca gcc agc tct gga ttt gtg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val 965 970 975	2928

gag gag aag tcc ctc agt gat gta gaa gaa gag gaa gct cct gaa gat Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro Glu Asp 980 985 990	2976
ctg tat aag gac ttc ctg acc ttg gag cat ctc atc tgt tac agc ttc Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe 995 1000 1005	3024
caa gtg gct aag ggc atg gag ttc ttg gca tcg cga aag tgt atc Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile 1010 1015 1020	3069
cac agg gac ctg gcg gca cga aat atc ctc tta tcg gag aag aac His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn 1025 1030 1035	3114
gtg gtt aaa atc tgt gac ttt ggc ttg gcc cgg gat att tat aaa Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys 1040 1045 1050	3159
gat cca gat tat gtc aga aaa gga gat gct cgc ctc cct ttg aaa Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys 1055 1060 1065	3204
tgg atg gcc cca gaa aca att ttt gac aga gtg tac aca atc cag Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln 1070 1075 1080	3249
agt gac gtc tgg tct ttt ggt gtt ttg ctg tgg gaa ata ttt tcc Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser 1085 1090 1095	3294
tta ggt gct tct cca tat cct ggg gta aag att gat gaa gaa ttt Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe 1100 1105 1110	3339
tgt agg cga ttg aaa gaa gga act aga atg agg gcc cct gat tat Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr 1115 1120 1125	3384
act aca cca gaa atg tac cag acc atg ctg gac tgc tgg cac ggg Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly 1130 1135 1140	3429
gag ccc agt cag aga ccc acg ttt tca gag ttg gtg gaa cat ttg Glu Pro Ser Gln Arg Pro Thr Phe Ser Glu Leu Val Glu His Leu 1145 1150 1155	3474
gga aat ctc ttg caa gct aat gct cag cag gat ggc aaa gac tac Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr 1160 1165 1170	3519
att gtt ctt ccg ata tca gag act ttg agc atg gaa gag gat tct Ile Val Leu Pro Ile Ser Glu Thr Leu Ser Met Glu Glu Asp Ser 1175 1180 1185	3564
gga ctc tct ctg cct acc tca cct gtt tcc tgt atg gag gag gag Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu 1190 1195 1200	3609
gaa gta tgt gac ccc aaa ttc cat tat gac aac aca gca gga atc Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile 1205 1210 1215	3654



agt cag tat ctg cag aac agt aag cga aag agc cgg cct gtg agt 3699  
 Ser Gln Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val Ser  
 1220 1225 1230  
  
 gta aaa aca ttt gaa gat atc ccg tta gaa gaa cca gaa gta aaa 3744  
 Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu Val Lys  
 1235 1240 1245  
  
 gta atc cca gat gac aac cag acg gac agt ggt atg gtt ctt gcc 3789  
 Val Ile Pro Asp Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala  
 1250 1255 1260  
  
 tca gaa gag ctg aaa act ttg gaa gac aga acc aaa tta tct cca 3834  
 Ser Glu Glu Leu Lys Thr Leu Glu Asp Arg Thr Lys Leu Ser Pro  
 1265 1270 1275  
  
 tct ttt ggt gga atg gtg ccc agc aaa agc agg gag tct gtg gca 3879  
 Ser Phe Gly Gly Met Val Pro Ser Lys Ser Arg Glu Ser Val Ala  
 1280 1285 1290  
  
 tct gaa ggc tca aac cag aca agc ggc tac cag tcc gga tat cac 3924  
 Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His  
 1295 1300 1305  
  
 tcc gat gac aca gac acc acc gtg tac tcc agt gag gaa gca gaa 3969  
 Ser Asp Asp Thr Asp Thr Val Tyr Ser Ser Glu Glu Ala Glu  
 1310 1315 1320  
  
 ctt tta aag ctg ata gag att gga gtg caa acc ggt agc aca gcc 4014  
 Leu Leu Lys Leu Ile Glu Ile Gly Val Gln Thr Gly Ser Thr Ala  
 1325 1330 1335  
  
 cag att ctc cag cct gac acg ggg acc aca ctg agc tct cct cct 4059  
 Gln Ile Leu Gln Pro Asp Thr Gly Thr Thr Leu Ser Ser Pro Pro  
 1340 1345 1350  
  
 gtt taa aaggaagcat ccacacccca actcccggac atcacatgag aggtctgctc 4115  
 Val  
  
 agatttttgaa gtgttgttct ttccaccagc aggaagtagc cgcatttgat tttcatttcg 4175  
  
 acaacagaaaa aaggacctcg gactgcaggg agccagctct tctaggcttg tgacc 4230

<210> 30  
 <211> 1354  
 <212> PRT  
 <213> Homo sapiens

<400> 30

Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu Thr Arg  
 1 5 10 15

Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro Arg Leu  
 20 25 30

Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr Leu Gln  
 35 40 45

Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Asn  
 50 55 60

Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser Asp Gly  
 65 70 75 80

Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn Asp Thr  
 85 90 95

Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser Val Ile  
 100 105 110

Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser  
 115 120 125

Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val  
 130 135 140

Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys  
 145 150 155 160

Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser  
 165 170 175

Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile Ser Tyr  
 180 185 190

Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser Tyr Gln  
 195 200 205

Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp Val  
 210 215 220

Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu  
 225 230 235 240

Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe  
 245 250 255

Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn  
 260 265 270

Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser  
 275 280 285

Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr  
 290 295 300

Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val  
 305 310 315 320  
 Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met Glu Ser  
 325 330 335  
 Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala Lys Tyr  
 340 345 350  
 Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly Ile Pro  
 355 360 365  
 Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr Ile Met  
 370 375 380  
 Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu Thr Asn  
 385 390 395 400  
 Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val Val Tyr  
 405 410 415  
 Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val Asp Ser  
 420 425 430  
 Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr Ala Ile  
 435 440 445  
 Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu Glu Cys  
 450 455 460  
 Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr Pro Cys  
 465 470 475 480  
 Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu  
 485 490 495  
 Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys Thr Val  
 500 505 510  
 Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys  
 515 520 525  
 Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser Phe His  
 530 535 540  
 Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln Pro Thr  
 545 550 555 560

Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser Thr Phe  
 565 570 575

Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro Ile His  
 580 585 590

Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr Leu Trp  
 595 600 605

Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile  
 610 615 620

Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys  
 625 630 635 640

Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val Arg Gln  
 645 650 655

Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn Leu Glu  
 660 665 670

Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys Thr Ala  
 675 680 685

Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn Glu Thr  
 690 695 700

Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg Asn Leu  
 705 710 715 720

Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr Cys Gln  
 725 730 735

Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe Ile Ile  
 740 745 750

Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu Val Gly  
 755 760 765

Thr Thr Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Ile Leu  
 770 775 780

Gly Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly Tyr Leu  
 785 790 795 800

Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His Cys Glu  
 805 810 815

Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu  
 820 825 830

Asn Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Glu Ile Glu  
 835 840 845

Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr Val Ala  
 850 855 860

Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu  
 865 870 875 880

Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val  
 885 890 895

Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val  
 900 905 910

Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Ser  
 915 920 925

Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg Phe Arg  
 930 935 940

Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys Arg Arg  
 945 950 955 960

Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val  
 965 970 975

Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro Glu Asp  
 980 985 990

Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe  
 995 1000 1005

Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile  
 1010 1015 1020

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn  
 1025 1030 1035

Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys  
 1040 1045 1050

Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys  
 1055 1060 1065

Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln  
 1070 1075 1080  
 Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser  
 1085 1090 1095  
 Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe  
 1100 1105 1110  
 Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr  
 1115 1120 1125  
 Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly  
 1130 1135 1140  
 Glu Pro Ser Gln Arg Pro Thr Phe Ser Glu Leu Val Glu His Leu  
 1145 1150 1155  
 Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr  
 1160 1165 1170  
 Ile Val Leu Pro Ile Ser Glu Thr Leu Ser Met Glu Glu Asp Ser  
 1175 1180 1185  
 Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu  
 1190 1195 1200  
 Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile  
 1205 1210 1215  
 Ser Gln Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val Ser  
 1220 1225 1230  
 Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu Val Lys  
 1235 1240 1245  
 Val Ile Pro Asp Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala  
 1250 1255 1260  
 Ser Glu Glu Leu Lys Thr Leu Glu Asp Arg Thr Lys Leu Ser Pro  
 1265 1270 1275  
 Ser Phe Gly Gly Met Val Pro Ser Lys Ser Arg Glu Ser Val Ala  
 1280 1285 1290  
 Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His  
 1295 1300 1305

Ser Asp Asp Thr Asp Thr Thr Val Tyr Ser Ser Glu Glu Ala Glu  
 1310 1315 1320

Leu Leu Lys Leu Ile Glu Ile Gly Val Gln Thr Gly Ser Thr Ala  
 1325 1330 1335

Gln Ile Leu Gln Pro Asp Thr Gly Thr Thr Leu Ser Ser Pro Pro  
 1340 1345 1350

Val

<210> 31  
 <211> 4195  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (20)..(3913)

<400> 31  
 ccacgcgcag cggccggag atg cag cgg ggc gcc gcg ctg tgc ctg cga ctg 52  
 Met Gln Arg Gly Ala Ala Leu Cys Leu Arg Leu  
 1 5 10

tgg ctc tgc ctg gga ctc ctg gac ggc ctg gtg agt ggc tac tcc atg 100  
 Trp Leu Cys Leu Gly Leu Leu Asp Gly Leu Val Ser Gly Tyr Ser Met  
 15 20 25

acc ccc ccg acc ttg aac atc acg gag gag tca cac gtc atc gac acc 148  
 Thr Pro Pro Thr Leu Asn Ile Thr Glu Glu Ser His Val Ile Asp Thr  
 30 35 40

ggt gac agc ctg tcc atc tcc tgc agg gga cag cac ccc ctc gag tgg 196  
 Gly Asp Ser Leu Ser Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp  
 45 50 55

gct tgg cca gga gct cag gag gcg cca gcc acc gga gac aag gac agc 244  
 Ala Trp Pro Gly Ala Gln Glu Ala Pro Ala Thr Gly Asp Lys Asp Ser  
 60 65 70 75

gag gac acg ggg gtg gtg cga gac tgc gag ggc aca gac gcc agg ccc 292  
 Glu Asp Thr Gly Val Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro  
 80 85 90

tac tgc aag gtg ttg ctg ctg cac gag gta cat gcc aac gac aca ggc 340  
 Tyr Cys Lys Val Leu Leu Leu His Glu Val His Ala Asn Asp Thr Gly  
 95 100 105

agc tac gtc tgc tac tac aag tac atc aag gca cgc atc gag ggc acc 388  
 Ser Tyr Val Cys Tyr Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr  
 110 115 120

acg gcc gcc agc tcc tac gtg ttc gtg aga gac ttt gag cag cca ttc 436  
 Thr Ala Ala Ser Ser Tyr Val Phe Val Arg Asp Phe Glu Gln Pro Phe  
 125 130 135

atc aac aag cct gac acg ctc ttg gtc aac agg aag gac gcc atg tgg 484  
 Ile Asn Lys Pro Asp Thr Leu Leu Val Asn Arg Lys Asp Ala Met Trp  
 140 145 150 155

gtg ccc tgt ctg gtg tcc atc ccc ggc ctc aat gtc acg ctg cgc tcg	532
Val Pro Cys Leu Val Ser Ile Pro Gly Leu Asn Val Thr Leu Arg Ser	
160 165 170	
caa agc tcg gtg ctg tgg cca gac ggg cag gag gtg gtg tgg gat gac	580
Gln Ser Ser Val Leu Trp Pro Asp Gly Gln Glu Val Val Trp Asp Asp	
175 180 185	
cgg cgg ggc atg ctc gtg tcc acg cca ctg ctg cac gat gcc ctg tac	628
Arg Arg Gly Met Leu Val Ser Thr Pro Leu Leu His Asp Ala Leu Tyr	
190 195 200	
ctg cag tgc gag acc acc tgg gga gac cag gac ttc ctt tcc aac ccc	676
Leu Gln Cys Glu Thr Thr Trp Gly Asp Gln Asp Phe Leu Ser Asn Pro	
205 210 215	
ttc ctg gtg cac atc aca ggc aac gag ctc tat gac atc cag ctg ttg	724
Phe Leu Val His Ile Thr Gly Asn Glu Leu Tyr Asp Ile Gln Leu Leu	
220 225 230 235	
ccc agg aag tcg ctg gag ctg ctg gta ggg gag aag ctg gtc ctg aac	772
Pro Arg Lys Ser Leu Glu Leu Leu Val Gly Glu Lys Leu Val Leu Asn	
240 245 250	
tgc acc gtg tgg gct gag ttt aac tca ggt gtc acc ttt gac tgg gac	820
Cys Thr Val Trp Ala Glu Phe Asn Ser Gly Val Thr Phe Asp Trp Asp	
255 260 265	
tac cca ggg aag cag gca gag cgg ggt aag tgg gtg ccc gag cga cgc	868
Tyr Pro Gly Lys Gln Ala Glu Arg Gly Lys Trp Val Pro Glu Arg Arg	
270 275 280	
tcc cag cag acc cac aca gaa ctc tcc agc atc ctg acc atc cac aac	916
Ser Gln Gln Thr His Thr Glu Leu Ser Ser Ile Leu Thr Ile His Asn	
285 290 295	
gtc agc cag cac gac ctg ggc tcg tat gtg tgc aag gcc aac aac ggc	964
Val Ser Gln His Asp Leu Gly Ser Tyr Val Cys Lys Ala Asn Asn Gly	
300 305 310 315	
atc cag cga ttt cgg gag agc acc gag gtc att gtg cat gaa aat ccc	1012
Ile Gln Arg Phe Arg Glu Ser Thr Glu Val Ile Val His Glu Asn Pro	
320 325 330	
ttc atc agc gtc gag tgg ctc aaa gga ccc atc ctg gag gcc acg gca	1060
Phe Ile Ser Val Glu Trp Leu Lys Gly Pro Ile Leu Glu Ala Thr Ala	
335 340 345	
gga gac gag ctg gtg aag ctg ccc gtg aag ctg gca gcg tac ccc ccg	1108
Gly Asp Glu Leu Val Lys Leu Pro Val Lys Leu Ala Ala Tyr Pro Pro	
350 355 360	
ccc gag ttc cag tgg tac aag gat gga aag gca ctg tcc ggg cgc cac	1156
Pro Glu Phe Gln Trp Tyr Lys Asp Gly Lys Ala Leu Ser Gly Arg His	
365 370 375	
agt cca cat gcc ctg gtg ctc aag gag gtg aca gag gcc agc aca ggc	1204
Ser Pro His Ala Leu Val Leu Lys Glu Val Thr Glu Ala Ser Thr Gly	
380 385 390 395	



acc tac acc ctc gcc ctg tgg aac tcc gct gct ggc ctg agg cgc aac	1252
Thr Tyr Thr Leu Ala Leu Trp Asn Ser Ala Ala Gly Leu Arg Arg Asn	
400 405 410	
atc agc ctg gag ctg gtg gtg aat gtg ccc ccc cag ata cat gag aag	1300
Ile Ser Leu Glu Leu Val Val Asn Val Pro Pro Gln Ile His Glu Lys	
415 420 425	
gag gcc tcc tcc ccc agc atc tac tgc cgt cac agc cgc cag gcc ctc	1348
Glu Ala Ser Ser Pro Ser Ile Tyr Ser Arg His Ser Arg Gln Ala Leu	
430 435 440	
acc tgc acg gcc tac ggg gtg ccc ctg cct ctc agc atc cag tgg cac	1396
Thr Cys Thr Ala Tyr Gly Pro Leu Pro Leu Ser Ile Gln Trp His	
445 450 455	
tgg cgg ccc tgg aca ccc tgc aag atg ttt gcc cag cgt agt ctc cgg	1444
Trp Arg Pro Trp Thr Pro Cys Lys Met Phe Ala Gln Arg Ser Leu Arg	
460 465 470 475	
cgg cgg cag cag caa gac ctc atg cca cag tgc cgt gac tgg agg gcg	1492
Arg Arg Gln Gln Gln Asp Leu Met Pro Gln Cys Arg Asp Trp Arg Ala	
480 485 490	
gtg acc acg cag gat gcc gtg aac ccc atc gag agc ctg gac acc tgg	1540
Val Thr Thr Gln Asp Ala Val Asn Pro Ile Glu Ser Leu Asp Thr Trp	
495 500 505	
acc gag ttt gtg gag gga aag aat aag act gtg agc aag ctg gtg atc	1588
Thr Glu Phe Val Glu Gly Lys Asn Lys Thr Val Ser Lys Leu Val Ile	
510 515 520	
cag aat gcc aac gtg tct gcc atg tac aag tgt gtg gtc tcc aac aag	1636
Gln Asn Ala Asn Val Ser Ala Met Tyr Lys Cys Val Val Ser Asn Lys	
525 530 535	
gtg ggc cag gat gag cgg ctc atc tac ttc tat gtg acc acc atc ccc	1684
Val Gly Gln Asp Glu Arg Leu Ile Tyr Phe Tyr Val Thr Thr Ile Pro	
540 545 550 555	
gac ggc ttc acc atc gaa tcc aag cca tcc gag gag cta cta gag ggc	1732
Asp Gly Phe Thr Ile Glu Ser Lys Pro Ser Glu Glu Leu Leu Glu Gly	
560 565 570	
cag ccg gtg ctc ctg agc tgc caa gcc gac agc tac aag tac gag cat	1780
Gln Pro Val Leu Leu Ser Cys Gln Ala Asp Ser Tyr Lys Tyr Glu His	
575 580 585	
ctg cgc tgg tac cgc ctc aac ctg tcc acg ctg cac gat gcg cac ggg	1828
Leu Arg Trp Tyr Arg Leu Asn Leu Ser Thr Leu His Asp Ala His Gly	
590 595 600	
aac ccg ctt ctg ctc gac tgc aag aac gtg cat ctg ttc gcc acc cct	1876
Asn Pro Leu Leu Leu Asp Cys Lys Asn Val His Leu Phe Ala Thr Pro	
605 610 615	
ctg gcc gcc agc ctg gag gag gtg gca cct ggg gcg cgc cac gcc acg	1924
Leu Ala Ala Ser Leu Glu Glu Val Ala Pro Gly Ala Arg His Ala Thr	
620 625 630 635	
ctc agc ctg agt atc ccc cgc gtc gcg ccc gag cac gag gcc cac tat	1972
Leu Ser Leu Ser Ile Pro Arg Val Ala Pro Glu His Glu Gly His Tyr	
640 645 650	

gtg tgc gaa gtg caa gac cgg cgc agc cat gac aag cac tgc cac aag	2020
Val Cys Glu Val Gln Asp Arg Arg Ser His Asp Lys His Cys His Lys	
655 660 665	
aag tac ctg tgc gtg cag gcc ctg gaa gcc cct cgg ctc acg cag aac	2068
Lys Tyr Leu Ser Val Gln Ala Leu Glu Ala Pro Arg Leu Thr Gln Asn	
670 675 680	
ttg acc gac ctc ctg gtg aac gtg agc gac tcg ctg gag atg cag tgc	2116
Leu Thr Asp Leu Leu Val Asn Val Ser Asp Ser Leu Glu Met Gln Cys	
685 690 695	
ttg gtg gcc gga gcg cac gcg ccc agc atc gtg tgg tac aaa gac gag	2164
Leu Val Ala Gly Ala His Ala Pro Ser Ile Val Trp Tyr Lys Asp Glu	
700 705 710 715	
agg ctg ctg gag gaa aag tct gga gtc gac ttg gcg gac tcc aac cag	2212
Arg Leu Leu Glu Glu Lys Ser Gly Val Asp Leu Ala Asp Ser Asn Gln	
720 725 730	
aag ctg agc atc cag cgc gtg cgc gag gag gat gcg gga cgc tat ctg	2260
Lys Leu Ser Ile Gln Arg Val Arg Glu Glu Asp Ala Gly Arg Tyr Leu	
735 740 745	
tgc agc gtg tgc aac gcc aag ggc tgc gtc aac tcc tcc gcc agc gtg	2308
Cys Ser Val Cys Asn Ala Lys Gly Cys Val Asn Ser Ser Ala Ser Val	
750 755 760	
gcc gtg gaa ggc tcc gag gat aag ggc agc atg gag atc gtg atc ctt	2356
Ala Val Glu Gly Ser Glu Asp Lys Gly Ser Met Glu Ile Val Ile Leu	
765 770 775	
gtc ggt acc ggc gtc atc gct gtc ttc ttc tgg gtc ctc ctc ctc ctc	2404
Val Gly Thr Gly Val Ile Ala Val Phe Phe Trp Val Leu Leu Leu Leu	
780 785 790 795	
atc ttc tgt aac atg agg agg ccg gcc cac gca gac atc aag acg ggc	2452
Ile Phe Cys Asn Met Arg Arg Pro Ala His Ala Asp Ile Lys Thr Gly	
800 805 810	
tac ctg tcc atc atc atg gac ccc ggg gag gtg cct ctg gag gag caa	2500
Tyr Leu Ser Ile Ile Met Asp Pro Gly Glu Val Pro Leu Glu Glu Gln	
815 820 825	
tgc gaa tac ctg tcc tac gat gcc agc cag tgg gaa ttc ccc cga gag	2548
Cys Glu Tyr Leu Ser Tyr Asp Ala Ser Gln Trp Glu Phe Pro Arg Glu	
830 835 840	
cgg ctg cac ctg ggg aga gtg ctc ggc tac ggc gcc ttc ggg aag gtg	2596
Arg Leu His Leu Gly Arg Val Leu Gly Tyr Gly Ala Phe Gly Lys Val	
845 850 855	
gtg gaa gcc tcc gct ttc ggc atc cac aag ggc agc agc tgt gac acc	2644
Val Glu Ala Ser Ala Phe Gly Ile His Lys Gly Ser Ser Cys Asp Thr	
860 865 870 875	
gtg gcc gtg aaa atg ctg aaa gag ggc gcc acg gcc agc gag cac cgc	2692
Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr Ala Ser Glu His Arg	
880 885 890	
gcg ctg atg tcg gag ctc aag atc ctc att cac atc ggc aac cac ctc	2740
Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly Asn His Leu	
895 900 905	

aac gtg gtc aac ctc ctc ggg gcg tgc acc aag ccg cag ggc ccc ctc 2788  
 Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gln Gly Pro Leu  
 910 915 920

atg gtg atc gtg gag ttc tgc aag tac ggc aac ctc tcc aac ttc ctg 2836  
 Met Val Ile Val Glu Phe Cys Lys Tyr Gly Asn Leu Ser Asn Phe Leu  
 925 930 935

cgc gcc aag cgg gac gcc ttc agc ccc tgc gcg gag aag tct ccc gag 2884  
 Arg Ala Lys Arg Asp Ala Phe Ser Pro Cys Ala Glu Lys Ser Pro Glu  
 940 945 950 955

cag cgc gga cgc ttc cgc gcc atg gtg gag ctc gcc agg ctg gat cgg 2932  
 Gln Arg Gly Arg Phe Arg Ala Met Val Glu Leu Ala Arg Leu Asp Arg  
 960 965 970

agg cgg ccg ggg agc agc gac agg gtc ctc ttc gcg cgg ttc tcg aag 2980  
 Arg Arg Pro Gly Ser Ser Asp Arg Val Leu Phe Ala Arg Phe Ser Lys  
 975 980 985

acc gag ggc gga gcg agg cgg gct tct cca gac caa gaa gct gag gac 3028  
 Thr Glu Gly Gly Ala Arg Arg Ala Ser Pro Asp Gln Glu Ala Glu Asp  
 990 995 1000

ctg tgg ctg agc ccg ctg acc atg gaa gat ctt gtc tgc tac agc ttc 3076  
 Leu Trp Leu Ser Pro Leu Thr Met Glu Asp Leu Val Cys Tyr Ser Phe  
 1005 1010 1015

cag gtg gcc aga ggg atg gag ttc ctg gct tcc cga aag tgc atc cac 3124  
 Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His  
 1020 1025 1030 1035

aga gac ctg gct gct cgg aac att ctg ctg tcg gaa agc gac gtg gtg 3172  
 Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Ser Asp Val Val  
 1040 1045 1050

aag atc tgt gac ttt ggc ctt gcc cgg gac atc tac aaa gac cct gac 3220  
 Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp  
 1055 1060 1065

tac gtc cgc aag ggc agt gcc cgg ctg ccc ctg aag tgg atg gcc cct 3268  
 Tyr Val Arg Lys Gly Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro  
 1070 1075 1080

gaa agc atc ttc gac aag gtg tac acc acg cag agt gac gtg tgg tcc 3316  
 Glu Ser Ile Phe Asp Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser  
 1085 1090 1095

ttt ggg gtg ctt ctc tgg gag atc ttc tct ctg ggg gcc tcc ccg tac 3364  
 Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr  
 1100 1105 1110 1115

cct ggg gtg cag atc aat gag gag ttc tgc cag cgg ctg aga gac ggc 3412  
 Pro Gly Val Gln Ile Asn Glu Glu Phe Cys Gln Arg Leu Arg Asp Gly  
 1120 1125 1130

aca agg atg agg gcc ccg gag ctg gcc act ccc gcc ata cgc cgc atc 3460  
 Thr Arg Met Arg Ala Pro Glu Leu Ala Thr Pro Ala Ile Arg Arg Ile  
 1135 1140 1145

atg ctg aac tgc tgg tcc gga gac ccc aag gcg aga cct gca ttc tcg 3508  
 Met Leu Asn Cys Trp Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser  
 1150 1155 1160

gag ctg gtg gag atc ctg ggg gac ctg ctc cag ggc agg ggc ctg caa 3556  
 Glu Leu Val Glu Ile Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln  
 1165 1170 1175

gag gaa gag gag gtc tgc atg gcc ccg cgc agc tct cag agc tca gaa 3604  
 Glu Glu Glu Glu Val Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu  
 1180 1185 1190 1195

gag ggc agc ttc tgc cag gtg tcc acc atg gcc cta cac atc gcc cag 3652  
 Glu Gly Ser Phe Ser Gln Val Ser Thr Met Ala Leu His Ile Ala Gln  
 1200 1205 1210

gct gac gct gag gac agc ccg cca agc ctg cag cgc cac agc ctg gcc 3700  
 Ala Asp Ala Glu Asp Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala  
 1215 1220 1225

gcc agg tat tac aac tgg gtg tcc ttt ccc ggg tgc ctg gcc aga ggg 3748  
 Ala Arg Tyr Tyr Asn Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly  
 1230 1235 1240

gct gag acc cgt ggt tcc tcc agg atg aag aca ttt gag gaa ttc ccc 3796  
 Ala Glu Thr Arg Gly Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro  
 1245 1250 1255

atg acc cca acg acc tac aaa ggc tct gtg gac aac cag aca gac agt 3844  
 Met Thr Pro Thr Thr Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser  
 1260 1265 1270 1275

ggg atg gtg ctg gcc tgc gag gag ttt gag cag ata gag agc agg cat 3892  
 Gly Met Val Leu Ala Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His  
 1280 1285 1290

aga caa gaa agc ggc ttc agg tagctgaagc agagagagag aaggcagcat 3943  
 Arg Gln Glu Ser Gly Phe Arg  
 1295

acgtcagcat tttcttctct gcacttataa gaaagatcaa agactttaag actttcgcta 4003  
 tttcttctac tgctatctac tacaaacttc aaagaggaac caggaggaca agaggagcat 4063  
 gaaagtggac aaggagtgtg accactgaag caccacaggg aaggggttag gcctccggat 4123  
 gactgcgggc aggctggat aatatccagc ctcccacaag aagctggtgg agcagagtgt 4183  
 tccctgactc ct 4195

<210> 32  
 <211> 1298  
 <212> PRT  
 <213> Homo sapiens

<400> 32  
 Met Gln Arg Gly Ala Ala Leu Cys Leu Arg Leu Trp Leu Cys Leu Gly  
 1 5 10 15

Leu Leu Asp Gly Leu Val Ser Gly Tyr Ser Met Thr Pro Pro Thr Leu  
 20 25 30

Asn Ile Thr Glu Glu Ser His Val Ile Asp Thr Gly Asp Ser Leu Ser  
 35 40 45

Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Ala Trp Pro Gly Ala  
 50 55 60

Gln Glu Ala Pro Ala Thr Gly Asp Lys Asp Ser Glu Asp Thr Gly Val  
 65 70 75 80

Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro Tyr Cys Lys Val Leu  
 85 90 95

Leu Leu His Glu Val His Ala Asn Asp Thr Gly Ser Tyr Val Cys Tyr  
 100 105 110

Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr Thr Ala Ala Ser Ser  
 115 120 125

Tyr Val Phe Val Arg Asp Phe Glu Gln Pro Phe Ile Asn Lys Pro Asp  
 130 135 140

Thr Leu Leu Val Asn Arg Lys Asp Ala Met Trp Val Pro Cys Leu Val  
 145 150 155 160

Ser Ile Pro Gly Leu Asn Val Thr Leu Arg Ser Gln Ser Ser Val Leu  
 165 170 175

Trp Pro Asp Gly Gln Glu Val Val Trp Asp Asp Arg Arg Gly Met Leu  
 180 185 190

Val Ser Thr Pro Leu Leu His Asp Ala Leu Tyr Leu Gln Cys Glu Thr  
 195 200 205

Thr Trp Gly Asp Gln Asp Phe Leu Ser Asn Pro Phe Leu Val His Ile  
 210 215 220

Thr Gly Asn Glu Leu Tyr Asp Ile Gln Leu Leu Pro Arg Lys Ser Leu  
 225 230 235 240

Glu Leu Leu Val Gly Glu Lys Leu Val Leu Asn Cys Thr Val Trp Ala  
 245 250 255

Glu Phe Asn Ser Gly Val Thr Phe Asp Trp Asp Tyr Pro Gly Lys Gln  
 260 265 270

Ala Glu Arg Gly Lys Trp Val Pro Glu Arg Arg Ser Gln Gln Thr His  
 275 280 285

Thr Glu Leu Ser Ser Ile Leu Thr Ile His Asn Val Ser Gln His Asp  
 290 295 300

Leu Gly Ser Tyr Val Cys Lys Ala Asn Asn Gly Ile Gln Arg Phe Arg  
 305 310 315 320

Glu Ser Thr Glu Val Ile Val His Glu Asn Pro Phe Ile Ser Val Glu  
 325 330 335

Trp Leu Lys Gly Pro Ile Leu Glu Ala Thr Ala Gly Asp Glu Leu Val  
 340 345 350

Lys Leu Pro Val Lys Leu Ala Ala Tyr Pro Pro Pro Glu Phe Gln Trp  
 355 360 365

Tyr Lys Asp Gly Lys Ala Leu Ser Gly Arg His Ser Pro His Ala Leu  
 370 375 380

Val Leu Lys Glu Val Thr Glu Ala Ser Thr Gly Thr Tyr Thr Leu Ala  
 385 390 395 400

Leu Trp Asn Ser Ala Ala Gly Leu Arg Arg Asn Ile Ser Leu Glu Leu  
 405 410 415

Val Val Asn Val Pro Pro Gln Ile His Glu Lys Glu Ala Ser Ser Pro  
 420 425 430

Ser Ile Tyr Ser Arg His Ser Arg Gln Ala Leu Thr Cys Thr Ala Tyr  
 435 440 445

Gly Val Pro Leu Pro Leu Ser Ile Gln Trp His Trp Arg Pro Trp Thr  
 450 455 460

Pro Cys Lys Met Phe Ala Gln Arg Ser Leu Arg Arg Arg Gln Gln Gln  
 465 470 475 480

Asp Leu Met Pro Gln Cys Arg Asp Trp Arg Ala Val Thr Thr Gln Asp  
 485 490 495

Ala Val Asn Pro Ile Glu Ser Leu Asp Thr Trp Thr Glu Phe Val Glu  
 500 505 510

Gly Lys Asn Lys Thr Val Ser Lys Leu Val Ile Gln Asn Ala Asn Val  
 515 520 525

Ser Ala Met Tyr Lys Cys Val Val Ser Asn Lys Val Gly Gln Asp Glu  
 530 535 540

Arg Leu Ile Tyr Phe Tyr Val Thr Thr Ile Pro Asp Gly Phe Thr Ile  
 545 550 555 560

Glu Ser Lys Pro Ser Glu Glu Leu Leu Glu Gly Gln Pro Val Leu Leu  
 565 570 575

Ser Cys Gln Ala Asp Ser Tyr Lys Tyr Glu His Leu Arg Trp Tyr Arg  
 580 585 590

Leu Asn Leu Ser Thr Leu His Asp Ala His Gly Asn Pro Leu Leu Leu  
 595 600 605

Asp Cys Lys Asn Val His Leu Phe Ala Thr Pro Leu Ala Ala Ser Leu  
 610 615 620

Glu Glu Val Ala Pro Gly Ala Arg His Ala Thr Leu Ser Leu Ser Ile  
 625 630 635 640

Pro Arg Val Ala Pro Glu His Glu Gly His Tyr Val Cys Glu Val Gln  
 645 650 655

Asp Arg Arg Ser His Asp Lys His Cys His Lys Lys Tyr Leu Ser Val  
 660 665 670

Gln Ala Leu Glu Ala Pro Arg Leu Thr Gln Asn Leu Thr Asp Leu Leu  
 675 680 685

Val Asn Val Ser Asp Ser Leu Glu Met Gln Cys Leu Val Ala Gly Ala  
 690 695 700

His Ala Pro Ser Ile Val Trp Tyr Lys Asp Glu Arg Leu Leu Glu Glu  
 705 710 715 720

Lys Ser Gly Val Asp Leu Ala Asp Ser Asn Gln Lys Leu Ser Ile Gln  
 725 730 735

Arg Val Arg Glu Glu Asp Ala Gly Arg Tyr Leu Cys Ser Val Cys Asn  
 740 745 750

Ala Lys Gly Cys Val Asn Ser Ser Ala Ser Val Ala Val Glu Gly Ser  
 755 760 765

Glu Asp Lys Gly Ser Met Glu Ile Val Ile Leu Val Gly Thr Gly Val  
 770 775 780

Ile Ala Val Phe Phe Trp Val Leu Leu Leu Leu Ile Phe Cys Asn Met  
 785 790 795 800

Arg Arg Pro Ala His Ala Asp Ile Lys Thr Gly Tyr Leu Ser Ile Ile  
805 810 815

Met Asp Pro Gly Glu Val Pro Leu Glu Glu Gln Cys Glu Tyr Leu Ser  
820 825 830

Tyr Asp Ala Ser Gln Trp Glu Phe Pro Arg Glu Arg Leu His Leu Gly  
835 840 845

Arg Val Leu Gly Tyr Gly Ala Phe Gly Lys Val Val Glu Ala Ser Ala  
850 855 860

Phe Gly Ile His Lys Gly Ser Ser Cys Asp Thr Val Ala Val Lys Met  
865 870 875 880

Leu Lys Glu Gly Ala Thr Ala Ser Glu His Arg Ala Leu Met Ser Glu  
885 890 895

Leu Lys Ile Leu Ile His Ile Gly Asn His Leu Asn Val Val Asn Leu  
900 905 910

Leu Gly Ala Cys Thr Lys Pro Gln Gly Pro Leu Met Val Ile Val Glu  
915 920 925

Phe Cys Lys Tyr Gly Asn Leu Ser Asn Phe Leu Arg Ala Lys Arg Asp  
930 935 940

Ala Phe Ser Pro Cys Ala Glu Lys Ser Pro Glu Gln Arg Gly Arg Phe  
945 950 955 960

Arg Ala Met Val Glu Leu Ala Arg Leu Asp Arg Arg Arg Pro Gly Ser  
965 970 975

Ser Asp Arg Val Leu Phe Ala Arg Phe Ser Lys Thr Glu Gly Gly Ala  
980 985 990

Arg Arg Ala Ser Pro Asp Gln Glu Ala Glu Asp Leu Trp Leu Ser Pro  
995 1000 1005

Leu Thr Met Glu Asp Leu Val Cys Tyr Ser Phe Gln Val Ala Arg Gly  
1010 1015 1020

Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala  
1025 1030 1035 1040

Arg Asn Ile Leu Leu Ser Glu Ser Asp Val Val Lys Ile Cys Asp Phe



1045	1050	1055
Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly 1060 1065 1070		
Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp 1075 1080 1085		
Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu 1090 1095 1100		
Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile 1105 1110 1115 1120		
Asn Glu Glu Phe Cys Gln Arg Leu Arg Asp Gly Thr Arg Met Arg Ala 1125 1130 1135		
Pro Glu Leu Ala Thr Pro Ala Ile Arg Arg Ile Met Leu Asn Cys Trp 1140 1145 1150		
Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Glu Leu Val Glu Ile 1155 1160 1165		
Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln Glu Glu Glu Val 1170 1175 1180		
Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser 1185 1190 1195 1200		
Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp 1205 1210 1215		
Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn 1220 1225 1230		
Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly 1235 1240 1245		
Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr 1250 1255 1260		
Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala 1265 1270 1275 1280		
Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly 1285 1290 1295		

Phe Arg

<210> 33  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 33

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr  
 1 5 10

<210> 34  
 <211> 18  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic primer

<400> 34  
 tccggtttcc tgtgaggc 18

<210> 35  
 <211> 18  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic primer

<400> 35  
 aagttgggta acgccagg 18

<210> 36  
 <211> 15  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic primer

<400> 36  
 tgacctcgcc cccgt 15

<210> 37  
 <211> 3088  
 <212> DNA  
 <213> Homo sapiens

<400> 37  
 ccccttttcc agaatacactt gcactgtctt gttcttgaat gagaaaggaa gaaaagagcc 60  
 tcccattact cagacccgtg taaacattat tccccccagg agaaaatggg gttattcaaa 120  
 tgaatcataa taaaatagcc tctaaacagt ttctaagcgg gagcctccgt ggaactcagc 180  
 gtcgccgtcc tcccagttcc taagaggtcc cgggattctt gagctgtgcc cagctgacga 240

gcttttgaag atggcacaat aaccgtccag tgatgcctga ccatgacagc acagccctct	300
taagccggca aaccaagagg agaagagttg acattggagt gaaaaggacg gtagggacag	360
catctgcatt ttttgctaag gcaagagcaa cgtttttttag tgccatgaat cccaaggtt	420
ctgagcagga tgttgagtat tcagtgggtgc agcatgcaga tggggaaaag tcaaattgtac	480
tccgcaagct gctgaagagg gcgaactcgt atgaagatgc catgatgcct tttccaggag	540
caaccataat ttcccagctg ttgaaaaata acatgaacaa aaatgggtggc acggagccca	600
gtttccaagc cagcgggtctc tctagtacag gctccgaagt acatcaggag gatatatgca	660
gcaactcttc aagagacagc cccccagagt gtctttcccc ttttggcagg cctactatga	720
gccagtttga tatggatcgc ttatgtgatg agcacctgag agcaaagcgc gcccggttg	780
agaatataat tcgggggtatg agccattccc ccagtgtggc attaaggggc aatgaaaatg	840
aaagagagat ggccccgcag tctgtgagtc cccgagaaaag ttacagagaa aacaaacgca	900
agcaaaagct tccccagcag cagcaacaga gtttccagca gctggtttca gcccgaaaag	960
aacagaagcg agaggagcgc cgacagctga aacagcagct ggaggacatg cagaaacagc	1020
tgcgccagct gcaggaaaaag ttctaccaa tctatgacag cactgattcg gaaaatgatg	1080
aagatggtaa cctgtctgaa gacagcatgc gctcggagat cctggatgcc agggcccagg	1140
actctgtcgg aaggtcagat aatgagatgt gcgagctaga cccaggacag tttattgacc	1200
gagctcgagc cctgatcaga gagcaggaaa tggctgaaaa caagccgaag cgagaaggca	1260
acaacaaaga aagagaccat gggccaaact ccttacaacc ggaaggcaaa cathttggctg	1320
agaccttgaa acaggaactg aacactgcc a tgctgcaagt tgtggacact gtggtcaaag	1380
tcttttcggc caagccctcc cgccagggttc ctcagggtctt cccacctctc cagatcccc	1440
aggccagatt tgcagtcaat ggggaaaacc acaatttcca caccgccaac cagcgcctgc	1500
agtgccttgg cgacgtcatc attccgaacc ccttgagcac ctttggcaat gtgcagatgg	1560
ccagttccac tgaccagaca gaagcactgc ccttggttgt ccgcaaaaac tcctctgacc	1620
agtctgcctc cgccctgcc gctggcgccc accaccagcc cctgcaccag tcgcctctct	1680
ctgccaccac gggcttcacc acgtccacct tccgccaccc cttccccctt cccttgatgg	1740
cctatccatt tcagagccca ttaggtgctc cctccggctc cttctctgga aaagacagag	1800
cctctcctga atccttagac ttaactaggg ataccacgag tctgaggacc aagatgtcat	1860
ctcaccacct gagccaccac ccttggtcac cagcacaccc gccagcacc gccgaagggc	1920
tctccttgct gctcataaag tccgagtgcg gcgatcttca agatatgtct gaaatatcac	1980
cttattcggg aagtgcaatg caggaaggat tgtcacccaa tcacttgaaa aaagcaaagc	2040
tcatgttttt ttatacccgt tatcccagct ccaatatgct gaagacctac ttctccgacg	2100
taaagttcaa cagatgcatt acctctcagc tcatcaagtg gtttagcaat ttccgtgagt	2160

```

tttactacat tcagatggag aagtacgcac gtcaagccat caacgatggg gtcaccagta 2220
ctgaagagct gtctataacc agagactgtg agctgtacag ggctctgaac atgcactaca 2280
ataaagcaaa tgactttgag gttccagaga gattcctgga agttgctcag atcacattac 2340
gggagttttt caatgccatt atcgcaggca aagatgttga tccttcctgg aagaaggcca 2400
tatacaaggt catctgcaag ctggatagtg aagtccctga gattttcaaa tccccgaact 2460
gcctacaaga gctgcttcat gagtagaaat ttcaacaact ctttttgaat gtatgaagag 2520
tagcagtccc ctttggatgt ccaagttata tgtgtctaga ttttgatttc atatatatgt 2580
gtatgggagg catggatatg ttatgaaatc agctggtaat tcctcctcat cacgtttctc 2640
tcattttctt ttgttttcca ttgcaagggg atggttggtt tctttctgcc tttagtttgc 2700
ttttgcccac ggcccttaac atttggacac ttaaaatagg gttaattttc agggaaaaag 2760
aatgttggcg tgtgtaaagt ctctattagc aatgaaggga atttggttaac gatgcatcca 2820
cttgattgat gacttattgc aaatggcggg tggctgagga aaacccatga cacagcacia 2880
ctctacagac agtgatgtgt ctcttgtttc tactgctaag aaggtctgaa aatttaatga 2940
aaccacttca tacatttaag tattttgttt ggtttgaact caatcagtag cttttcctta 3000
catgtttaaa aataattcca atgacagatg agcagctcac ttttccaaag taccocaaaa 3060
ggccaaatta aaaaaaaaaa aaaaaaaaaa 3088

```

&lt;210&gt; 38

&lt;211&gt; 737

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

```

Met Pro Asp His Asp Ser Thr Ala Leu Leu Ser Arg Gln Thr Lys Arg
1          5          10          15

```

```

Arg Arg Val Asp Ile Gly Val Lys Arg Thr Val Gly Thr Ala Ser Ala
          20          25          30

```

```

Phe Phe Ala Lys Ala Arg Ala Thr Phe Phe Ser Ala Met Asn Pro Gln
          35          40          45

```

```

Gly Ser Glu Gln Asp Val Glu Tyr Ser Val Val Gln His Ala Asp Gly
          50          55          60

```

```

Glu Lys Ser Asn Val Leu Arg Lys Leu Leu Lys Arg Ala Asn Ser Tyr
          65          70          75          80

```

```

Glu Asp Ala Met Met Pro Phe Pro Gly Ala Thr Ile Ile Ser Gln Leu
          85          90          95

```

Leu Lys Asn Asn Met Asn Lys Asn Gly Gly Thr Glu Pro Ser Phe Gln  
 100 105 110

Ala Ser Gly Leu Ser Ser Thr Gly Ser Glu Val His Gln Glu Asp Ile  
 115 120 125

Cys Ser Asn Ser Ser Arg Asp Ser Pro Pro Glu Cys Leu Ser Pro Phe  
 130 135 140

Gly Arg Pro Thr Met Ser Gln Phe Asp Met Asp Arg Leu Cys Asp Glu  
 145 150 155 160

His Leu Arg Ala Lys Arg Ala Arg Val Glu Asn Ile Ile Arg Gly Met  
 165 170 175

Ser His Ser Pro Ser Val Ala Leu Arg Gly Asn Glu Asn Glu Arg Glu  
 180 185 190

Met Ala Pro Gln Ser Val Ser Pro Arg Glu Ser Tyr Arg Glu Asn Lys  
 195 200 205

Arg Lys Gln Lys Leu Pro Gln Gln Gln Gln Gln Ser Phe Gln Gln Leu  
 210 215 220

Val Ser Ala Arg Lys Glu Gln Lys Arg Glu Glu Arg Arg Gln Leu Lys  
 225 230 235 240

Gln Gln Leu Glu Asp Met Gln Lys Gln Leu Arg Gln Leu Gln Glu Lys  
 245 250 255

Phe Tyr Gln Ile Tyr Asp Ser Thr Asp Ser Glu Asn Asp Glu Asp Gly  
 260 265 270

Asn Leu Ser Glu Asp Ser Met Arg Ser Glu Ile Leu Asp Ala Arg Ala  
 275 280 285

Gln Asp Ser Val Gly Arg Ser Asp Asn Glu Met Cys Glu Leu Asp Pro  
 290 295 300

Gly Gln Phe Ile Asp Arg Ala Arg Ala Leu Ile Arg Glu Gln Glu Met  
 305 310 315 320

Ala Glu Asn Lys Pro Lys Arg Glu Gly Asn Asn Lys Glu Arg Asp His  
 325 330 335

Gly Pro Asn Ser Leu Gln Pro Glu Gly Lys His Leu Ala Glu Thr Leu  
 340 345 350

Lys Gln Glu Leu Asn Thr Ala Met Ser Gln Val Val Asp Thr Val Val  
 355 360 365

Lys Val Phe Ser Ala Lys Pro Ser Arg Gln Val Pro Gln Val Phe Pro  
 370 375 380

Pro Leu Gln Ile Pro Gln Ala Arg Phe Ala Val Asn Gly Glu Asn His  
 385 390 395 400

Asn Phe His Thr Ala Asn Gln Arg Leu Gln Cys Phe Gly Asp Val Ile  
 405 410 415

Ile Pro Asn Pro Leu Asp Thr Phe Gly Asn Val Gln Met Ala Ser Ser  
 420 425 430

Thr Asp Gln Thr Glu Ala Leu Pro Leu Val Val Arg Lys Asn Ser Ser  
 435 440 445

Asp Gln Ser Ala Ser Gly Pro Ala Ala Gly Gly His His Gln Pro Leu  
 450 455 460

His Gln Ser Pro Leu Ser Ala Thr Thr Gly Phe Thr Thr Ser Thr Phe  
 465 470 475 480

Arg His Pro Phe Pro Leu Pro Leu Met Ala Tyr Pro Phe Gln Ser Pro  
 485 490 495

Leu Gly Ala Pro Ser Gly Ser Phe Ser Gly Lys Asp Arg Ala Ser Pro  
 500 505 510

Glu Ser Leu Asp Leu Thr Arg Asp Thr Thr Ser Leu Arg Thr Lys Met  
 515 520 525

Ser Ser His His Leu Ser His His Pro Cys Ser Pro Ala His Pro Pro  
 530 535 540

Ser Thr Ala Glu Gly Leu Ser Leu Ser Leu Ile Lys Ser Glu Cys Gly  
 545 550 555 560

Asp Leu Gln Asp Met Ser Glu Ile Ser Pro Tyr Ser Gly Ser Ala Met  
 565 570 575

Gln Glu Gly Leu Ser Pro Asn His Leu Lys Lys Ala Lys Leu Met Phe  
 580 585 590

Phe Tyr Thr Arg Tyr Pro Ser Ser Asn Met Leu Lys Thr Tyr Phe Ser  
 595 600 605

Asp Val Lys Phe Asn Arg Cys Ile Thr Ser Gln Leu Ile Lys Trp Phe  
 610 615 620

Ser Asn Phe Arg Glu Phe Tyr Tyr Ile Gln Met Glu Lys Tyr Ala Arg  
 625 630 635 640

Gln Ala Ile Asn Asp Gly Val Thr Ser Thr Glu Glu Leu Ser Ile Thr  
 645 650 655

Arg Asp Cys Glu Leu Tyr Arg Ala Leu Asn Met His Tyr Asn Lys Ala  
 660 665 670

Asn Asp Phe Glu Val Pro Glu Arg Phe Leu Glu Val Ala Gln Ile Thr  
 675 680 685

Leu Arg Glu Phe Phe Asn Ala Ile Ile Ala Gly Lys Asp Val Asp Pro  
 690 695 700

Ser Trp Lys Lys Ala Ile Tyr Lys Val Ile Cys Lys Leu Asp Ser Glu  
 705 710 715 720

Val Pro Glu Ile Phe Lys Ser Pro Asn Cys Leu Gln Glu Leu Leu His  
 725 730 735

Glu